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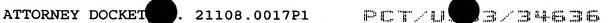
SEQUENCE LISTING

<110> University of Rochester

      Chang, Chawnshang

<120> Hydroxyflutamide Induced Pathways
      Related to Androgen Receptor Negative Prostate Cancer Cells

<130> 21108.0017P1

<150> 60/423,340
<151> 2002-10-31

<150> PCT/US02/11086
<151> 2002-04-05

<150> 60/365,060
<151> 2002-03-13

<150> 60/282,266
<151> 2001-04-06

<160> 28

<170> FastSEQ for Windows Version 4.0

<210> 1
<211> 1587
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:/note =
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<400> 1
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actgggggaa aaatcacttt ccagtctgtt ttgcaaggtg tgcatttcca tcttgattcc   120
ctgaaagtcc atctgctgca tcggtcaaga gaaactccac ttgcatgaag attgcacgcc   180
tgcagcttgc atctttgttg caaaactagc tacagaagag aagcaaggca aagtcttttg   240
tgctcccctc ccccatcaaa ggaaaggga aaatgtctca gtcgaaaggc aagaagcgaa   300
accctggcct taaaattcca aaagaagcat ttgaacaacc tcagaccagt tccacaccac   360
ctagagattt agactccaag gcttgcattt ctattggaaa tcagaacttt gaggtgaagg   420
cagatgacct ggagcctata atggaactgg gacgaggtgc gtacggggtg gtggagaaga   480
tgcggcacgt gcccagcggg cagatcatgg cagtgaagcg gatccgagcc acagtaaata   540
gccaggaaca gaaacggcta ctgatggatt tggatatttc catgaggacg gtggactgtc   600
cattcactgt caccttttat ggcgcactgt ttcgggaggg tgatgtgtgg atctgcatgg   660
agctcatgga tacatcacta gataaattct acaaacaagt tattgataaa ggccagacaa   720
ttccagagga catcttaggg aaaatagcag tttctattgt aaaagcatta gaacatttac   780
atagtaagct gtctgtcatt cacagagacg tcaagccttc taatgtactc atcaatgctc   840
tcggtcaagt gaagatgtgc gattttggaa tcagtggcta cttggtggac tctgttgcta   900
aaacaattga tgcaggttgc aaaccataca tggcccctga aagaataaac ccagagctca   960
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tggtagagga gccatcgcca caactcccag cagacaagtt ctctgcagag tttgttgact   1140
ttacctcaca gtgcttaaag aagaattcca aagaacggcc tacataccca gagctaatgc   1200
aacatccatt tttcacccta catgaatcca aaggaacaga tgtggcatct tttgtaaaac   1260
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1

```
gtttcggggt gaagcaagtt cactacagca tcaatagaaa gtcatctttg agataattta      1380
accctgcctc tcagagggtt ttctctccca attttctttt tactccccct cttaaggggg      1440
ccttggaatc tatagtatag aatgaactgt ctagatggat gaattatgat aaaggcttag      1500
gacttcaaaa ggtgattaaa tatttaatga tgtgtcatat gaaaaaaaaa aaaaaaaaaa      1560
aaaaaaaaaa aaaaaaaaaa aaaaaaa                                         1587
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<210> 2
<211> 334
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:/note =
      synthetic construct

<400> 2

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Lys Glu Ala Phe Glu Gln Pro Gln Thr Ser Ser Thr Pro Pro Arg Asp
                20                  25                  30
Leu Asp Ser Lys Ala Cys Ile Ser Ile Gly Asn Gln Asn Phe Glu Val
            35                  40                  45
Lys Ala Asp Asp Leu Glu Pro Ile Met Glu Leu Gly Arg Gly Ala Tyr
        50                  55                  60
Gly Val Val Glu Lys Met Arg His Val Pro Ser Gly Gln Ile Met Ala
65                  70                  75                  80
Val Lys Arg Ile Arg Ala Thr Val Asn Ser Gln Glu Gln Lys Arg Leu
                85                  90                  95
Leu Met Asp Leu Asp Ile Ser Met Arg Thr Val Asp Cys Pro Phe Thr
                100                 105                 110
Val Thr Phe Tyr Gly Ala Leu Phe Arg Glu Gly Asp Val Trp Ile Cys
            115                 120                 125
Met Glu Leu Met Asp Thr Ser Leu Asp Lys Phe Tyr Lys Gln Val Ile
        130                 135                 140
Asp Lys Gly Gln Thr Ile Pro Glu Asp Ile Leu Gly Lys Ile Ala Val
145                 150                 155                 160
Ser Ile Val Lys Ala Leu Glu His Leu His Ser Lys Leu Ser Val Ile
                165                 170                 175
His Arg Asp Val Lys Pro Ser Asn Val Leu Ile Asn Ala Leu Gly Gln
            180                 185                 190
Val Lys Met Cys Asp Phe Gly Ile Ser Gly Tyr Leu Val Asp Ser Val
        195                 200                 205
Ala Lys Thr Ile Asp Ala Gly Cys Lys Pro Tyr Met Ala Pro Glu Arg
        210                 215                 220
Ile Asn Pro Glu Leu Asn Gln Lys Gly Tyr Ser Val Lys Ser Asp Ile
225                 230                 235                 240
Trp Ser Leu Gly Ile Thr Met Ile Glu Leu Ala Ile Leu Arg Phe Pro
                245                 250                 255
Tyr Asp Ser Trp Gly Thr Pro Phe Gln Gln Leu Lys Gln Val Val Glu
            260                 265                 270
Glu Pro Ser Pro Gln Leu Pro Ala Asp Lys Phe Ser Ala Glu Phe Val
        275                 280                 285
Asp Phe Thr Ser Gln Cys Leu Lys Lys Asn Ser Lys Glu Arg Pro Thr
        290                 295                 300
Tyr Pro Glu Leu Met Gln His Pro Phe Phe Thr Leu His Glu Ser Lys
305                 310                 315                 320
Gly Thr Asp Val Ala Ser Phe Val Lys Leu Ile Leu Gly Asp
                325                 330
```

<210> 3
<211> 3080
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:/note =
      synthetic construct

<400> 3
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agccagccca ttgacatccc agatgccaag aagagaggcc ggaaaaagaa gcgctgtcgg     120
gctactgaca gcttctcagg caggttcgaa gatgtctatc agctgcagga ggatgtgctg     180
ggggaaggtg ctcacgctcg tgtgcagacc tgtgtcaatc tcatcaccaa ccaggaatat     240
gctgtcaaga tcattgagaa gcagctgggc cacatccgca gcagggtgtt ccgggaggtg     300
gagatgctgt accagtgcca gggacatagg aatgttctag aactgattga gttctttgag     360
gaggaggacc gtttctacct ggtgtttgag aagatgcgtg gcggatccat cctaagccac     420
atccatagaa ggcgccactt taacgagctg gaggccagcg tggtagtaca ggacgtggcc     480
agtgccctgg acttcctgca taacaaaggc atcgcccaca gggacctaaa gccagagaac     540
atcctatgtg agcaccccaa ccaggtctcg ccagtgaaga tctgcgactt cgaccttggc     600
agtggtatca aactcaatgg agactgctcc cccatctcca caccagagct gctcaccccg     660
tgtgggtcag ctgagtacat ggccccagag gtggtggagg ccttcagtga gaggccagc      720
atctacgaca gcgctgcga cctgtggagc ctgggcgtca tcctctacat cctgcttagt     780
ggctacccgc ccttcgtggg ccactgtggc agcgactgtg gctgggaccg tggggaggcc     840
tgtcctgcct gccagaacat gctgtttgag agcatccagg agggcaagta tgagttccct     900
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tgtgccccag agaacaccct accgacaccc ttggttctgc agaggaacag ctgtgccaaa    1080
gacctcacgt cctttgcggc tgaggccatc gccatgaacc ggcagctggc ccagtgtgag    1140
gaggacgctg ggcaggacca gcctgtggtc atccgagcta cctcacgctg cctgcagctg    1200
tccccaccct cccagtccaa gctggcccag cggcgccaga gggctagcct gtcggccacc    1260
cctgtggtcc ttgtggggga tcgcgcatga cccccactag ctccttgtac atatgcccct    1320
gccccgcggg gcctgaaggc tagggacctg gacaccccac cccttgccat tccaggtgcc    1380
agctcagctg ggtcctctgg gggtgtaggg gtctgttagg gggtgtctcc ttttctccct    1440
gtccttcccc tgccctgccc acttggcttt gttttgtttg ttttctttg ccgctattga    1500
aagcaagtgc ccggaggagg gcggagggct caggccgccc agcctgcacc ccacgatgct    1560
cacctgccaa ctgtgaaggt cctgccacct gcgcccccac ctccactcca gccactctgc    1620
tgtcttccag ggttggggat cccgcagggt cagcacccca cacctctccc agccctcagt    1680
gttgtcaggg acaggccctc ctggtgagca cagtggtggt tgcatctcct caccagagca    1740
cccttgggtc tggggtaggg cagggctccc tgtcttggat agagacctct ggggagcagg    1800
tggatgggga cagtgcactt gattgacccc gagtccccat catccacctg cagtgtccct    1860
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ctactgctcc caacccact tcccaggggc agagctggaa ggggaccctg cacccagcta    1980
gctccaccac agcaggagag gtgctggacc aggctttcat cagcaaacat ggggctccca    2040
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acgtcctgcc cctggggttc ctaagctctc ctagctgctt ctgttagcca gagctgaggc    2160
catacccagg gctctcacct tcctgttgcc cccagagggc agcagctcag gcgtgcctgc    2220
tttcaggaaa gggaggctgg gaagggatgt ggtggccctg cggtgccag acctaactgc     2280
ccgaggcctg tagactgttc tagccgaact actatgcaat acaagttccc attttctcca    2340
tggccctgct ggtcggggc ggctgccagg gccaggcca ccctgccctg caactgctca     2400
ggtgtctaca gggcagcccc tggcctcaaa aatccttggt caggattgtt tgtcgagttt    2460
agtttaggct tttttttttt ttttaaagaa ataatttgac ttgcttccct gttcttgaag    2520
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tgggggacat gcaagcactt ttaactccat cgtaccaggt gaactgacct ccggactcct    3000
ttcccaccaa ctgtcaacgc caggattttg tattctgttt tgtaaggatt taataaaagt    3060
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catttaaaaa aaaaaaaaaa   3080

<210> 4
<211> 412
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:/note =
      synthetic construct

<400> 4
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 1               5                  10                  15
Arg Lys Lys Lys Arg Cys Arg Ala Thr Asp Ser Phe Ser Gly Arg Phe
            20                  25                  30
Glu Asp Val Tyr Gln Leu Gln Glu Asp Val Leu Gly Glu Gly Ala His
         35                  40                  45
Ala Arg Val Gln Thr Cys Val Asn Leu Ile Thr Asn Gln Glu Tyr Ala
      50                  55                  60
Val Lys Ile Ile Glu Lys Gln Leu Gly His Ile Arg Ser Arg Val Phe
65                  70                  75                  80
Arg Glu Val Glu Met Leu Tyr Gln Cys Gln Gly His Arg Asn Val Leu
                85                  90                  95
Glu Leu Ile Glu Phe Phe Glu Glu Glu Asp Arg Phe Tyr Leu Val Phe
               100                 105                 110
Glu Lys Met Arg Gly Gly Ser Ile Leu Ser His Ile His Arg Arg Arg
           115                 120                 125
His Phe Asn Glu Leu Glu Ala Ser Val Val Val Gln Asp Val Ala Ser
       130                 135                 140
Ala Leu Asp Phe Leu His Asn Lys Gly Ile Ala His Arg Asp Leu Lys
145                 150                 155                 160
Pro Glu Asn Ile Leu Cys Glu His Pro Asn Gln Val Ser Pro Val Lys
                165                 170                 175
Ile Cys Asp Phe Asp Leu Gly Ser Gly Ile Lys Leu Asn Gly Asp Cys
               180                 185                 190
Ser Pro Ile Ser Thr Pro Glu Leu Leu Thr Pro Cys Gly Ser Ala Glu
           195                 200                 205
Tyr Met Ala Pro Glu Val Val Glu Ala Phe Ser Glu Glu Ala Ser Ile
       210                 215                 220
Tyr Asp Lys Arg Cys Asp Leu Trp Ser Leu Gly Val Ile Leu Tyr Ile
225                 230                 235                 240
Leu Leu Ser Gly Tyr Pro Pro Phe Val Gly His Cys Gly Ser Asp Cys
               245                 250                 255
Gly Trp Asp Arg Gly Glu Ala Cys Pro Ala Cys Gln Asn Met Leu Phe
           260                 265                 270
Glu Ser Ile Gln Glu Gly Lys Tyr Glu Phe Pro Asp Lys Asp Trp Ser
           275                 280                 285
His Ile Ser Phe Ala Ala Lys Asp Leu Ile Ser Lys Leu Leu Val Arg
       290                 295                 300
Asp Ala Lys Gln Arg Leu Ser Ala Ala Gln Val Leu Gln His Pro Trp
305                 310                 315                 320
Val Gln Gly Cys Ala Pro Glu Asn Thr Leu Pro Thr Pro Leu Val Leu
               325                 330                 335
Gln Arg Asn Ser Cys Ala Lys Asp Leu Thr Ser Phe Ala Ala Glu Ala
           340                 345                 350
Ile Ala Met Asn Arg Gln Leu Ala Gln Cys Glu Glu Asp Ala Gly Gln
       355                 360                 365
Asp Gln Pro Val Val Ile Arg Ala Thr Ser Arg Cys Leu Gln Leu Ser
       370                 375                 380
```

4

```
Pro Pro Ser Gln Ser Lys Leu Ala Gln Arg Arg Gln Arg Ala Ser Leu
385             390             395             400
Ser Ala Thr Pro Val Val Leu Val Gly Asp Arg Ala
            405             410
```

<210> 5
<211> 1096
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:/note =
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<400> 5
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cttcttgctc agtgccctga agtttctctg caatgaactg acaaatcgga accatggtgc    180
aaaagaagtt ctgccctcgg ttacttgact atctcgtgat cgtaggggcg aggcacccaa    240
gcagtgacag tgtggctcag actcctgagc tgctgcggag gtacccacta gaggatcacc    300
cagagttccc cctgccccca gatgtggtgt tcttctgcca gccagaagga tgtctgagtg    360
tgcggcagcg gcggatgagc cttcgggacg atacctcttt tgtcttcacc ctaaccgata    420
aggacaccgg agtcacccgc tatggcatct gtgtcaactt ctaccgttcc ttccaaaagc    480
gaatgccaaa ggaaaaggtg gaaggcggag caggaccccg tgggaaggaa ggcgctcaca    540
cctctggtgc ctcagaagag gctgccgctg ggagctcaga gagtggctca accttgcagc    600
cgcctagtgc tgactccact cctgacgtaa accagtctcc tcggggcaaa cgtagggcaa    660
aagcgggcag ccgctcccgc aacagtaccc tgacatccct gtgtgtgctt agccactacc    720
ctttcttctc taccttcaga gagtgtctgt atactctcaa acgtttggta gactgctgta    780
gtgaacggct gctaggcaag aaactgggca tccctcgagg tgtacaaagg tacggtttgc    840
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ttcccagcaa ttacatggtg gctcacaaca ttctgtaatg gggtcggatg ccctcttctg   1020
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aaaaaaaaaa aaaaaa                                                    1096
```

<210> 6
<211> 232
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:/note =
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<400> 6
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Met Val Gln Lys Lys Phe Cys Pro Arg Leu Leu Asp Tyr Leu Val Ile
1               5               10              15
Val Gly Ala Arg His Pro Ser Ser Asp Ser Val Ala Gln Thr Pro Glu
            20              25              30
Leu Leu Arg Arg Tyr Pro Leu Glu Asp His Pro Glu Phe Pro Leu Pro
        35              40              45
Pro Asp Val Val Phe Phe Cys Gln Pro Glu Gly Cys Leu Ser Val Arg
    50              55              60
Gln Arg Arg Met Ser Leu Arg Asp Asp Thr Ser Phe Val Phe Thr Leu
65              70              75              80
Thr Asp Lys Asp Thr Gly Val Thr Arg Tyr Gly Ile Cys Val Asn Phe
            85              90              95
Tyr Arg Ser Phe Gln Lys Arg Met Pro Lys Glu Lys Val Glu Gly Gly
            100             105             110
Ala Gly Pro Arg Gly Lys Glu Gly Ala His Thr Ser Gly Ala Ser Glu
        115             120             125
```

5

```
Glu Ala Ala Ala Gly Ser Ser Glu Ser Gly Ser Thr Leu Gln Pro Pro
    130             135             140
Ser Ala Asp Ser Thr Pro Asp Val Asn Gln Ser Pro Arg Gly Lys Arg
145             150             155             160
Arg Ala Lys Ala Gly Ser Arg Ser Arg Asn Ser Thr Leu Thr Ser Leu
            165             170             175
Cys Val Leu Ser His Tyr Pro Phe Phe Ser Thr Phe Arg Glu Cys Leu
            180             185             190
Tyr Thr Leu Lys Arg Leu Val Asp Cys Cys Ser Glu Arg Leu Leu Gly
        195             200             205
Lys Lys Leu Gly Ile Pro Arg Gly Val Gln Arg Tyr Gly Leu Leu Leu
    210             215             220
Val Leu Gly Arg Thr Leu Arg Asp
225             230
```

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<210> 7
<211> 7161
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:/note =
      synthetic construct

<400> 7
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aggggggccga gcgaatgtag cccgcgagag aaaatggcgg cggcggcggg gaatcgcgcc     180
tcgtcgtcgg gattcccggg cgccagggct acgagccctg aggcaggcgg cggcggagga     240
gccctcaagg cgagcagcgc gcccgcggct gccgcgggac tgctgcggga ggcgggcagc     300
ggggggccgcg agcgggcgga ctggcggcgg cggcagctgc gcaaagtgcg gagtgtggag     360
ctggaccagc tgcctgagca gccgctcttc cttgccgcct caccgccggc ctcctcgact     420
tccccgtcgc cggagcccgc ggacgcagcg gggagtggga ccggcttcca gcctgtggcg     480
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gccgccgagc cgtctcctgc agcggcccccc gccggtcgtg agatggagaa taaagaaact     660
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ccttcagacc caatgttatg gagaaaaact ttaaagaatt ttgaggttga gagtttgttc    1320
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atgcttgatg aagaaagtct tacagtgtgt gaagacggct gcaggaacaa gctgcaccac    1560
cactgcatgt caatttgggc agaagagtgt agaagaaata gagaaccttt aatatgtccc    1620
ctttgtagat ctaagtggag atctcatgat ttctacagcc acgagttgtc aagtcctgtg    1680
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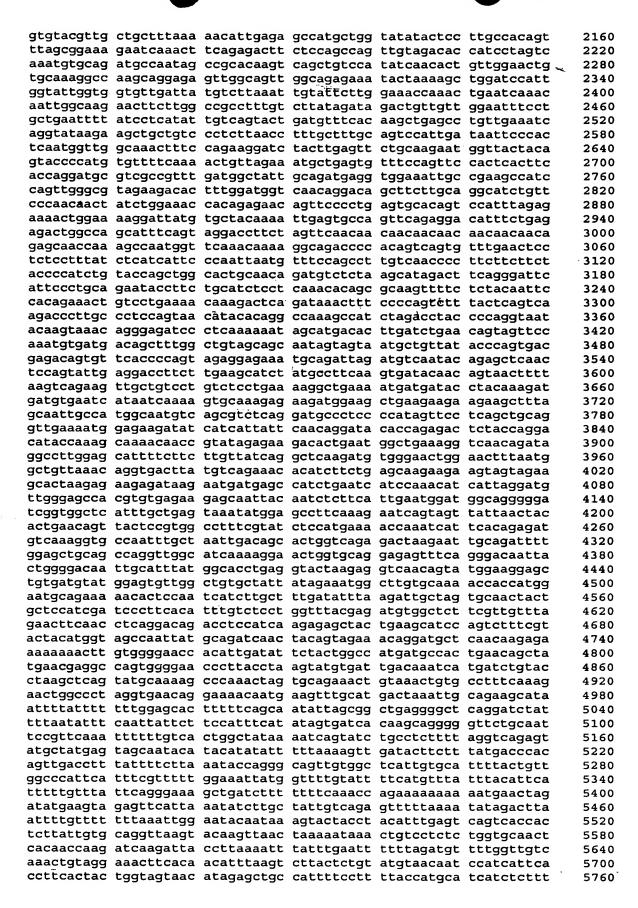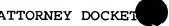
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ggtattggtg gtgttgatta tgtcttaaat tgtattcttg gaaaccaaac tgaatcaaac   2400
aattggcaag aacttcttgg ccgcctttgt cttatagata gactgttgtt ggaatttcct   2460
gctgaatttt atcctcatat tgtcagtact gatgtttcac aagctgagcc tgttgaaatc   2520
aggtataaga agctgctgtc cctcttaacc tttgctttgc agtccattga taattcccac   2580
tcaatggttg gcaaactttc cagaaggatc tacttgagtt ctgcaagaat ggttactaca   2640
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gagcaaccaa agccaatggt tcaaacaaaa ggcagacccc acagtcagtg tttgaactcc   3060
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<211> 1563
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:/note =
      synthetic construct

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                20                  25                  30
Ser Gly Arg Ala Gly Thr Trp Pro Arg Gly Pro Ser Glu Cys Ser Pro
            35                  40                  45
Arg Glu Lys Met Ala Ala Ala Ala Gly Asn Arg Ala Ser Ser Ser Gly
        50                  55                  60
Phe Pro Gly Ala Arg Ala Thr Ser Pro Glu Ala Gly Gly Gly Gly Gly
65                  70                  75                  80
Ala Leu Lys Ala Ser Ser Ala Pro Ala Ala Ala Ala Gly Leu Leu Arg
                85                  90                  95
Glu Ala Gly Ser Gly Gly Arg Glu Arg Ala Asp Trp Arg Arg Arg Gln
                100                 105                 110
Leu Arg Lys Val Arg Ser Val Glu Leu Asp Gln Leu Pro Glu Gln Pro
        115                 120                 125
Leu Phe Leu Ala Ala Ser Pro Pro Ala Ser Ser Thr Ser Pro Ser Pro
    130                 135                 140
Glu Pro Ala Asp Ala Ala Gly Ser Gly Thr Gly Phe Gln Pro Val Ala
145                 150                 155                 160
Val Pro Pro Pro His Gly Ala Ala Ser Arg Gly Gly Ala His Leu Thr
                165                 170                 175
Glu Ser Val Ala Ala Pro Asp Ser Gly Ala Ser Ser Pro Ala Ala Ala
                180                 185                 190
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Glu Pro Gly Glu Lys Arg Ala Pro Ala Ala Glu Pro Ser Pro Ala Ala
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Ala Pro Ala Gly Arg Glu Met Glu Asn Lys Glu Thr Leu Lys Gly Leu
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His Lys Met Asp Asp Arg Pro Glu Glu Arg Met Ile Arg Glu Lys Leu
225                 230                 235                 240
Lys Ala Thr Cys Met Pro Ala Trp Lys His Glu Trp Leu Glu Arg Arg
                245                 250                 255
Asn Arg Arg Gly Pro Val Val Val Lys Pro Ile Pro Val Lys Gly Asp
            260                 265                 270
Gly Ser Glu Met Asn His Leu Ala Ala Glu Ser Pro Gly Glu Val Gln
        275                 280                 285
Ala Ser Ala Ala Ser Pro Ala Ser Lys Gly Arg Arg Ser Pro Ser Pro
    290                 295                 300
Gly Asn Ser Pro Ser Gly Arg Thr Val Lys Ser Glu Ser Pro Gly Val
305                 310                 315                 320
Arg Arg Lys Arg Val Ser Pro Val Pro Phe Gln Ser Gly Arg Ile Thr
                325                 330                 335
Pro Pro Arg Arg Ala Pro Ser Pro Asp Gly Phe Ser Pro Tyr Ser Pro
            340                 345                 350
Glu Glu Thr Asn Arg Arg Val Asn Lys Val Met Arg Ala Arg Leu Tyr
        355                 360                 365
Leu Leu Gln Gln Ile Gly Pro Asn Ser Phe Leu Ile Gly Gly Asp Ser
    370                 375                 380
Pro Asp Asn Lys Tyr Arg Val Phe Ile Gly Pro Gln Asn Cys Ser Cys
385                 390                 395                 400
Ala Arg Gly Thr Phe Cys Ile His Leu Leu Phe Val Met Leu Arg Val
                405                 410                 415
Phe Gln Leu Glu Pro Ser Asp Pro Met Leu Trp Arg Lys Thr Leu Lys
            420                 425                 430
Asn Phe Glu Val Glu Ser Leu Phe Gln Lys Tyr His Ser Arg Arg Ser
        435                 440                 445
Ser Arg Ile Lys Ala Pro Ser Arg Asn Thr Ile Gln Lys Phe Val Ser
    450                 455                 460
Arg Met Ser Asn Ser His Thr Leu Ser Ser Ser Ser Thr Ser Thr Ser
465                 470                 475                 480
Ser Ser Glu Asn Ser Ile Lys Asp Glu Glu Glu Gln Met Cys Pro Ile
                485                 490                 495
Cys Leu Leu Gly Met Leu Asp Glu Glu Ser Leu Thr Val Cys Glu Asp
            500                 505                 510
Gly Cys Arg Asn Lys Leu His His His Cys Met Ser Ile Trp Ala Glu
        515                 520                 525
Glu Cys Arg Arg Asn Arg Glu Pro Leu Ile Cys Pro Leu Cys Arg Ser
    530                 535                 540
Lys Trp Arg Ser His Asp Phe Tyr Ser His Glu Leu Ser Ser Pro Val
545                 550                 555                 560
Asp Ser Pro Ser Ser Leu Arg Ala Ala Gln Gln Gln Thr Val Gln Gln
                565                 570                 575
Gln Pro Leu Ala Gly Ser Arg Arg Asn Gln Glu Ser Asn Phe Asn Leu
            580                 585                 590
Thr His Tyr Gly Thr Gln Gln Ile Pro Pro Ala Tyr Lys Asp Leu Ala
        595                 600                 605
Glu Pro Trp Ile Gln Val Phe Gly Met Glu Leu Val Gly Cys Leu Phe
    610                 615                 620
Ser Arg Asn Trp Asn Val Arg Glu Met Ala Leu Arg Arg Leu Ser His
625                 630                 635                 640
Asp Val Ser Gly Ala Leu Leu Leu Ala Asn Gly Glu Ser Thr Gly Asn
                645                 650                 655
Ser Gly Gly Ser Ser Gly Ser Ser Pro Ser Gly Gly Ala Thr Ser Gly
            660                 665                 670
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9

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Ser Ser Gln Thr Ser Ile Ser Gly Asp Val Val Glu Ala Cys Cys Ser
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Val Leu Ser Met Val Cys Ala Asp Pro Val Tyr Lys Val Tyr Val Ala
        690             695             700
Ala Leu Lys Thr Leu Arg Ala Met Leu Val Tyr Thr Pro Cys His Ser
705             710             715             720
Leu Ala Glu Arg Ile Lys Leu Gln Arg Leu Leu Gln Pro Val Val Asp
                725             730             735
Thr Ile Leu Val Lys Cys Ala Asp Ala Asn Ser Arg Thr Ser Gln Leu
                740             745             750
Ser Ile Ser Thr Leu Leu Glu Leu Cys Lys Gly Gln Ala Gly Glu Leu
                755             760             765
Ala Val Gly Arg Glu Ile Leu Lys Ala Gly Ser Ile Gly Ile Gly Gly
        770             775             780
Val Asp Tyr Val Leu Asn Cys Ile Leu Gly Asn Gln Thr Glu Ser Asn
785             790             795             800
Asn Trp Gln Glu Leu Leu Gly Arg Leu Cys Leu Ile Asp Arg Leu Leu
                805             810             815
Leu Glu Phe Pro Ala Glu Phe Tyr Pro His Ile Val Ser Thr Asp Val
                820             825             830
Ser Gln Ala Glu Pro Val Glu Ile Arg Tyr Lys Lys Leu Leu Ser Leu
        835             840             845
Leu Thr Phe Ala Leu Gln Ser Ile Asp Asn Ser His Ser Met Val Gly
        850             855             860
Lys Leu Ser Arg Arg Ile Tyr Leu Ser Ser Ala Arg Met Val Thr Thr
865             870             875             880
Val Pro His Val Phe Ser Lys Leu Leu Glu Met Leu Ser Val Ser Ser
                885             890             895
Ser Thr His Phe Thr Arg Met Arg Arg Arg Leu Met Ala Ile Ala Asp
        900             905             910
Glu Val Glu Ile Ala Glu Ala Ile Gln Leu Gly Val Glu Asp Thr Leu
        915             920             925
Asp Gly Gln Gln Asp Ser Phe Leu Gln Ala Ser Val Pro Asn Asn Tyr
    930             935             940
Leu Glu Thr Thr Glu Asn Ser Ser Pro Glu Cys Thr Val His Leu Glu
945             950             955             960
Lys Thr Gly Lys Gly Leu Cys Ala Thr Lys Leu Ser Ala Ser Ser Glu
                965             970             975
Asp Ile Ser Glu Arg Leu Ala Ser Ile Ser Val Gly Pro Ser Ser Ser
            980             985             990
Thr Thr Thr Thr Thr Thr Thr Thr Glu Gln Pro Lys Pro Met Val Gln
        995             1000            1005
Thr Lys Gly Arg Pro His Ser Gln Cys Leu Asn Ser Ser Pro Leu Ser
    1010            1015            1020
His His Ser Gln Leu Met Phe Pro Ala Leu Ser Thr Pro Ser Ser Ser
1025            1030            1035            1040
Thr Pro Ser Val Pro Ala Gly Thr Ala Thr Asp Val Ser Lys His Arg
                1045            1050            1055
Leu Gln Gly Phe Ile Pro Cys Arg Ile Pro Ser Ala Ser Pro Gln Thr
            1060            1065            1070
Gln Arg Lys Phe Ser Leu Gln Phe His Arg Asn Cys Pro Glu Asn Lys
        1075            1080            1085
Asp Ser Asp Lys Leu Ser Pro Val Phe Thr Gln Ser Arg Pro Leu Pro
    1090            1095            1100
Ser Ser Asn Ile His Arg Pro Lys Pro Ser Arg Pro Thr Pro Gly Asn
1105            1110            1115            1120
Thr Ser Lys Gln Gly Asp Pro Ser Lys Asn Ser Met Thr Leu Asp Leu
            1125            1130            1135
Asn Ser Ser Ser Lys Cys Asp Asp Ser Phe Gly Cys Ser Ser Asn Ser
        1140            1145            1150
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Ser Asn Ala Val Ile Pro Ser Asp Glu Thr Val Phe Thr Pro Val Glu
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Glu Lys Cys Arg Leu Asp Val Asn Thr Glu Leu Asn Ser Ser Ile Glu
        1170            1175            1180
Asp Leu Leu Glu Ala Ser Met Pro Ser Ser Asp Thr Thr Val Thr Phe
1185            1190            1195            1200
Lys Ser Glu Val Ala Val Leu Ser Pro Glu Lys Ala Glu Asn Asp Asp
            1205            1210        ·       1215
Thr Tyr Lys Asp Asp Val Asn His Asn Gln Lys Cys Lys Glu Lys Met
        1220            1225            1230
Glu Ala Glu Glu Glu Glu Ala Leu Ala Ile Ala Met Ala Met Ser Ala
        1235            1240            1245
Ser Gln Asp Ala Leu Pro Ile Val Pro Gln Leu Gln Val Glu Asn Gly
        1250            1255            1260
Glu Asp Ile Ile Ile Ile Gln Gln Asp Thr Pro Glu Thr Leu Pro Gly
1265            1270            1275            1280
His Thr Lys Ala Lys Gln Pro Tyr Arg Glu Asp Thr Glu Trp Leu Lys
            1285            1290        ·       1295
Gly Gln Gln Ile Gly Leu Gly Ala Phe Ser Ser Cys Tyr Gln Ala Gln
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Asp Val Gly Thr Gly Thr Leu Met Ala Val Lys Gln Val Thr Tyr Val
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Arg Asn Thr Ser Ser Glu Gln Glu Glu Val Val Glu Ala Leu Arg Glu
        1330            1335            1340
Glu Ile Arg Met Met Ser His Leu Asn His Pro Asn Ile Ile Arg Met
1345            1350            1355            1360
Leu Gly Ala Thr Cys Glu Lys Ser Asn Tyr Asn Leu Phe Ile Glu Trp
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Met Ala Gly Gly Ser Val Ala His Leu Leu Ser Lys Tyr Gly Ala Phe
            1380            1385            1390
Lys Glu Ser Val Val Ile Asn Tyr Thr Glu Gln Leu Leu Arg Gly Leu
        1395            1400            1405
Ser Tyr Leu His Glu Asn Gln Ile Ile His Arg Asp Val Lys Gly Ala
        1410            1415            1420    -
Asn Leu Leu Ile Asp Ser Thr Gly Gln Arg Leu Arg Ile Ala Asp Phe
1425            1430            1435            1440
Gly Ala Ala Ala Arg Leu Ala Ser Lys Gly Thr Gly Ala Gly Glu Phe
            1445            1450            1455
Gln Gly Gln Leu Leu Gly Thr Ile Ala Phe Met Ala Pro Glu Val Leu
            1460            1465            1470
Arg Gly Gln Gln Tyr Gly Arg Ser Cys Asp Val Trp Ser Val Gly Cys
        1475            1480            1485
Ala Ile Ile Glu Met Ala Cys Ala Lys Pro Pro Trp Asn Ala Glu Lys
        1490            1495            1500
His Ser Asn His Leu Ala Leu Ile Phe Lys Ile Ala Ser Ala Thr Thr
1505            1510            1515            1520
Ala Pro Ser Ile Pro Ser His Leu Ser Pro Gly Leu Arg Asp Val Ala
            1525            1530            1535
Leu Arg Cys Leu Glu Leu Gln Pro Gln Asp Arg Pro Pro Ser Arg Glu
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Leu Leu Lys His Pro Val Phe Arg Thr Thr Trp
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<211> 3621
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:/note =
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12

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aaagaaaaaa aaaaaaaaaa a                                                3621
```

<210> 10
<211> 657
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:/note =
      synthetic construct

<400> 10

```
Met Asp Glu Gln Glu Ala Leu Asn Ser Ile Met Asn Asp Leu Val Ala
 1           5                   10                  15
Leu Gln Met Asn Arg Arg His Arg Met Pro Gly Tyr Glu Thr Met Lys
            20                  25                  30
Asn Lys Asp Thr Gly His Ser Asn Arg Gln Lys Lys His Asn Ser Ser
            35                  40                  45
Ser Ser Ala Leu Leu Asn Ser Pro Thr Val Thr Thr Ser Ser Cys Ala
        50                  55                  60
Gly Ala Ser Glu Lys Lys Lys Phe Leu Ser Asp Val Arg Ile Lys Phe
65                  70                  75                  80
Glu His Asn Gly Glu Arg Arg Ile Ile Ala Phe Ser Arg Pro Val Lys
                85                  90                  95
Tyr Glu Asp Val Glu His Lys Val Thr Thr Val Phe Gly Gln Pro Leu
            100                 105                 110
Asp Leu His Tyr Met Asn Asn Glu Leu Ser Ile Leu Leu Lys Asn Gln
            115                 120                 125
Asp Asp Leu Asp Lys Ala Ile Asp Ile Leu Asp Arg Ser Ser Ser Met
            130                 135                 140
Lys Ser Leu Arg Ile Leu Leu Leu Ser Gln Asp Arg Asn His Asn Ser
145                 150                 155                 160
Ser Ser Pro His Ser Gly Val Ser Arg Gln Val Arg Ile Lys Ala Ser
                165                 170                 175
Gln Ser Ala Gly Asp Ile Asn Thr Ile Tyr Gln Pro Pro Glu Pro Arg
            180                 185                 190
Ser Arg His Leu Ser Val Ser Ser Gln Asn Pro Gly Arg Ser Ser Pro
            195                 200                 205
Pro Pro Gly Tyr Val Pro Glu Arg Gln Gln His Ile Ala Arg Gln Gly
    210                 215                 220
Ser Tyr Thr Ser Ile Asn Ser Glu Gly Glu Phe Ile Pro Glu Thr Ser
225                 230                 235                 240
Glu Gln Cys Met Leu Asp Pro Leu Ser Ser Ala Glu Asn Ser Leu Ser
                245                 250                 255
Gly Ser Cys Gln Ser Leu Asp Arg Ser Ala Asp Ser Pro Ser Phe Arg
            260                 265                 270
Lys Ser Arg Met Ser Arg Ala Gln Ser Phe Pro Asp Asn Arg Gln Glu
            275                 280                 285
Tyr Ser Asp Arg Glu Thr Gln Leu Tyr Asp Lys Gly Val Lys Gly Gly
    290                 295                 300
Thr Tyr Pro Arg Arg Tyr His Val Ser Val His His Lys Asp Tyr Ser
305                 310                 315                 320
Asp Gly Arg Arg Thr Phe Pro Arg Ile Arg Arg His Gln Gly Asn Leu
                325                 330                 335
Phe Thr Leu Val Pro Ser Ser Arg Ser Leu Ser Thr Asn Gly Glu Asn
            340                 345                 350
Met Gly Leu Ala Val Gln Tyr Leu Asp Pro Arg Gly Arg Leu Arg Ser
            355                 360                 365
Ala Asp Ser Glu Asn Ala Leu Ser Val Gln Glu Arg Asn Val Pro Thr
    370                 375                 380
```

13

<210> 13
<211> 444
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:/note =
     synthetic construct

<400> 13
ttcaaaagtg ttctgtttaa tacgctttgt ctggtagtgc ttgggtgcct gtggttggtt   60
tctctcactg gaaccagtcc tgggccccac tcgcctggct tcctccagtc gccccaggtc   120
ctggggctgg tgtgtcagaa gctgcctttg tcctctccat tcatccatcc ttgggcctgt   180
ctggcctatg atgccctcat tcagctctca gggtccagag gtgactggtg tggatcctgc   240
tcgctgtgcc aagatggccc tccagatgcg gcataccatc cctccctga tgcgggtgta   300
gatgaggtca tctcgagtgg cataggtgag cagagtgtgg agggtgaagc tatggttcaa   360
cagcatttgg atggtgcctg aatccacatt cagttcctgt agccactgca ccaggccctg   420
gtccgttgaa gaagcagtgg aggc   444

<210> 14
<211> 4693
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:/note =
     synthetic construct

<400> 14
ccgagccctg aggcaggcgg cggcggagga gccctcaagg cgagcagcgc gcgcgcggct   60
gccgcgggac tgctgcggga ggcgggcagc ggggggccgcg agcgggcgga ctggcggcgg   120
cggcagctgc gcaaagtgcg gagtgtggag ctggaccagc tgcctgagca gccgctcttc   180
cttgccgcct caccgccggc ctcctcgact tccccgtcgc cggagcccgc ggacgcagcg   240
gggagtggga ccggcttcca gcctgtggcg gtgccgccgc cccacggagc cgccagccgg   300
cgcggcgccc accttaccga gtcggtggcg gcgccggaca gcggcgcctc gagtcccgca   360
gcggccgagc ccggggagaa gcgggcgccc gccgccgagc cgtctcctgc agcggccccc   420
gccggtcgtg agatggagaa taaagaaact ctcaaagggt tgcacaagat ggatgatcgt   480
ccagaggaac gaatgatcag ggagaaactg aaggcaacct gtatgccagc ctggaagcac   540
gaatggttgg aaaggagaaa taggcgaggg cctgtggtgg taaaaccaat cccagttaaa   600
ggagatggat ctgaaatgaa tcacttagca gctgagtctc caggagaggt ccaggcaagt   660
gcggcttcac cagcttccaa aggccgacgc agtccttctc ctggcaactc cccatcaggt   720
cgcacagtga aatcagaatc tccaggagta aggagaaaaa gagtttcccc agtgcctttt   780
cagagtggca gaatcacacc accccgaaga gcccccttcac cagatggctt ctcaccatat   840
agccctgagg aaacaaaccg ccgtgttaac aaagtgatgc gggccagact gtacttactg   900
cagcagatag ggcctaactc tttcctgatt ggaggagaca gcccagacaa taaataccgg   960
gtgtttattg ggcctcagaa ctgcagctgt gcacatggaa cattctgtat tcatctgcta   1020
tttgtgatgc tccgggtgtt tcaactagaa ccttcagacc caatgttatg gagaaaaact   1080
ttaaagaatt ttgaggttga gagtttgttc cagaaatatc acagtaggcg tagctcaagg   1140
atcaaagctc catctcgtaa caccatccag aagtttgttt cacgcatgtc aaattctcat   1200
acattgtcat catctagtac ttctacatct agttcagaaa acagcataaa ggatgaagag   1260
gaacagatgt gtcctatttg cttgttgggc atgcttgatg aagaaagtct tacagtgtgt   1320
gaagacggct gcaggaacaa gctgcaccac cactgcatgt caatttgggc agaagagtgt   1380
agaagaaata gagaaccttt aatatgtccc ctttgtagat ctaagtggag atctcatgat   1440
ttctacagcc acgagttgtc aagtcctgtg gattcccctt cttccctcag agctgcacag   1500
cagcaaaccg tacagcagca gcctttggct ggatcacgaa ggaatcaaga gagcaatttt   1560
aaccttactc attatggaac tcagcaaatc cctcctgctt acaaagattt agctgagcca   1620
tggattcagg tgtttggaat ggaactcgtt ggctgcttat tttctagaaa ctggaatgtg   1680
agagagatgg ccctcaggcg tctttcccat gatgtcagtg gggccctgct gttggcaaat   1740
ggggagagca ctggaaattc tggggcagc agtggaagca gcccgagtgg gggagccacc   1800
agtgggtctt cccagaccag tatctcagga gatgtggtgg aggcatgctg cagcgttctg   1860
tcaatggtct gtgctgaccc tgtctacaaa gtgtacgttg ctgctttaaa aacattgaga   1920

```
gccatgctgg tatatactcc ttgccacagt ttagcggaaa gaatcaaact tcagagactt   1980
ctccagccag ttgtagacac catcctagtc aaatgtgcag atgccaatag ccgcacaagt   2040
cagctgtcca tatcaacact gttggaactg tgcaaaggcc aagcaggaga gttggcagtt   2100
ggcagagaaa tactaaaagc tggatccatt ggtattggtg gtgttgatta tgtcttaaat   2160
tgtattcttg gaaaccaaac tgaatcaaac aattggcaag aacttcttgg ccgcctttgt   2220
cttatagata gactgttgtt ggaatttcct gctgaatttt atcctcatat tgtcagtact   2280
gatgtttcac aagctgagcc tgttgaaatc aggtataaga agctgctgtc cctcttaacc   2340
tttgctttgc agtccattga taattcccac tcaatggttg gcaaactttc cagaaggatc   2400
tacttgagtt ctgcaagaat ggttactaca gtaccccatg tgtttttcaaa actgttagaa   2460
atgctgagtg tttccagtgt ttccactcac ttcaccagga tgcgtcgccg tttgatggct   2520
tatgcagatg aggtggaaat tgccgaagcc atccagttgg gcgtagaaga cactttacaa   2580
cgacaacaac acaacagctt ttgcaggcat ctgttcccaa caactatctg gaaaccacag   2640
agaacagttc cccttgagtg cacagtccat ttagagaaaa ctggaaaagg attatgtgct   2700
acaaaattga gtgccagttc agaggacatt tctgagagac tggccaggat ttcagtagga   2760
ccttctagtt caacaacaac aacaacaaca acaacagagc aaccaaagcc aatggttcaa   2820
acaaaaggca gaccccacag tcagtgtttg aactcctctc ctttatctca tcattcccaa   2880
ttaatgtttc cagccttgtc aacccttct  tcttctaccc catctgtacc agctggcact   2940
gcaacagatg tctctaagca tagacttcag ggattcattc cctgcagaat accttctgca   3000
tctcctcaaa cacagcgcaa gttttctcta caattccaca gaaactgtcc tgaaaacaaa   3060
gactcagata aactttcccc agtctttact cagtcaagac ccttgccctc cagtaacata   3120
cacaggccaa agccatctcg acctaccca ggtaatacaa gtaaacaggg agatccctca   3180
aaaaatagca tgacacttga tctgaacagt agttccaaat gtgatgacag ctttggcttg   3240
agcagcaata gtagtaattg ctgttatacc agtgacgaga cagtgttcac cccagtagag   3300
gagaaatgca gattagatgt caatacagag ctcaactcca gtattgagga ccttcttgaa   3360
gcatctatgc cttcaagtga tacaacagta acttttaagt cagaagttgc tgtcctgtct   3420
cctgaaaagg ctgaaaatga tgataccтac aaagatgatg tgaatcataa tcaaaagtgc   3480
aaagagaaga tggaagctga agaagaagaa gctttagcaa ttgccatggc aatgtcagcg   3540
tctcaggtag ccctcccat agttcctcag ctgcaggttg aaaatggaga agatatcatc   3600
attattcaac aggatacacc agagactcta ccaggacata ccaaagcaaa acaaccgtat   3660
agagaagaca ctgaatggct gaaaggtcaa cagataggcc ttggagcatt ttcttcttgt   3720
tatcaggctc aagatgtggg aactggaact ttaatggctg ttaaacaggt gacttatgtc   3780
agaaacacat cttctgagca agaagaagta gtagaagcac taagagaaga gataagaatg   3840
atgagccatc tgaatcatcc aaacatcatt aggatgttgg gagccacgtg tgagaagagc   3900
aattacaatc tcttcattga atggatggca gggggatcgg tggctcattt gctgagtaaa   3960
tatggagcct tcaaagaatc agtagtatt  aactacactg aacagttact ccgtggactt   4020
tcgtatctcc atgaaaacca aatcattcac agagatgtca aaggtgccaa tttgctaatt   4080
gacagcactg gtcagagact aagaattgca gattttggag ctgcagccag gttggcatca   4140
aaaggaactg gtgcaggaga gtttcaggga caattactgg ggacaattgc atttatggca   4200
cctgaggtac taagaggtca acagtatgga aggagctgtg atgtatggag tgttggctgt   4260
gctattatag aaatggcttg tgcaaaacca ccatggaatg cagaaaaaca ctccaatcat   4320
cttgctttga tatttaagat tgctagtgca actactgctc catcgatccc ttcacatttg   4380
tctcctggtt tacgagatgt ggctcttcgt tgtttagaac ttcaacctca ggacagacct   4440
ccatcaagag agctactgaa gcatccagtc tttcgtacta catggtagcc aattatacag   4500
atcaactacg tagaaacagg atgctcaaca agagaaaaaa aacttgtggg gaaccacatt   4560
gatatctacg gccatgatgc cactgaacag ctatgaacga ggccagtggg gaacccttac   4620
ctaagtatgt gattgacaaa tcatgatctg tacctaagct cagtatgcaa aagcccaaac   4680
tagtgcagaa act                                                       4693
```

```
<210> 15
<211> 1495
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:/note =
      synthetic construct

<400> 15
Pro Ser Pro Glu Ala Gly Gly Gly Gly Gly Ala Leu Lys Ala Ser Ser
1               5                   10                  15
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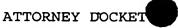
```
Ala Arg Ala Ala Ala Ala Gly Leu Leu Arg Glu Ala Gly Ser Gly Gly
        20              25              30
Arg Glu Arg Ala Asp Trp Arg Arg Arg Gln Leu Arg Lys Val Arg Ser
        35              40              45
Val Glu Leu Asp Gln Leu Pro Glu Gln Pro Leu Phe Leu Ala Ala Ser
    50              55              60
Pro Pro Ala Ser Ser Thr Ser Pro Ser Pro Glu Pro Ala Asp Ala Ala
65              70              75              80
Gly Ser Gly Thr Gly Phe Gln Pro Val Ala Val Pro Pro Pro His Gly
            85              90              95
Ala Ala Ser Arg Arg Gly Ala His Leu Thr Glu Ser Val Ala Ala Pro
        100             105             110
Asp Ser Gly Ala Ser Ser Pro Ala Ala Ala Glu Pro Gly Glu Lys Arg
        115             120             125
Ala Pro Ala Ala Glu Pro Ser Pro Ala Ala Ala Pro Ala Gly Arg Glu
        130             135             140
Met Glu Asn Lys Glu Thr Leu Lys Gly Leu His Lys Met Asp Asp Arg
145             150             155             160
Pro Glu Glu Arg Met Ile Arg Glu Lys Leu Lys Ala Thr Cys Met Pro
            165             170             175
Ala Trp Lys His Glu Trp Leu Glu Arg Arg Asn Arg Arg Gly Pro Val
        180             185             190
Val Val Lys Pro Ile Pro Val Lys Gly Asp Gly Ser Glu Met Asn His
        195             200             205
Leu Ala Ala Glu Ser Pro Gly Glu Val Gln Ala Ser Ala Ala Ser Pro
    210             215             220
Ala Ser Lys Gly Arg Arg Ser Pro Ser Pro Gly Asn Ser Pro Ser Gly
225             230             235             240
Arg Thr Val Lys Ser Glu Ser Pro Gly Val Arg Arg Lys Arg Val Ser
            245             250             255
Pro Val Pro Phe Gln Ser Gly Arg Ile Thr Pro Pro Arg Arg Ala Pro
            260             265             270
Ser Pro Asp Gly Phe Ser Pro Tyr Ser Pro Glu Glu Thr Asn Arg Arg
        275             280             285
Val Asn Lys Val Met Arg Ala Arg Leu Tyr Leu Leu Gln Gln Ile Gly
    290             295             300
Pro Asn Ser Phe Leu Ile Gly Gly Asp Ser Pro Asp Asn Lys Tyr Arg
305             310             315             320
Val Phe Ile Gly Pro Gln Asn Cys Ser Cys Ala His Gly Thr Phe Cys
            325             330             335
Ile His Leu Leu Phe Val Met Leu Arg Val Phe Gln Leu Glu Pro Ser
        340             345             350
Asp Pro Met Leu Trp Arg Lys Thr Leu Lys Asn Phe Glu Val Glu Ser
        355             360             365
Leu Phe Gln Lys Tyr His Ser Arg Arg Ser Ser Arg Ile Lys Ala Pro
    370             375             380
Ser Arg Asn Thr Ile Gln Lys Phe Val Ser Arg Met Ser Asn Ser His
385             390             395             400
Thr Leu Ser Ser Ser Ser Thr Ser Thr Ser Ser Glu Asn Ser Ile
            405             410             415
Lys Asp Glu Glu Glu Gln Met Cys Pro Ile Cys Leu Leu Gly Met Leu
        420             425             430
Asp Glu Glu Ser Leu Thr Val Cys Glu Asp Gly Cys Arg Asn Lys Leu
        435             440             445
His His His Cys Met Ser Ile Trp Ala Glu Glu Cys Arg Arg Asn Arg
    450             455             460
Glu Pro Leu Ile Cys Pro Leu Cys Arg Ser Lys Trp Arg Ser His Asp
465             470             475             480
Phe Tyr Ser His Glu Leu Ser Ser Pro Val Asp Ser Pro Ser Ser Leu
            485             490             495
```

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```
Arg Ala Ala Gln Gln Gln Thr Val Gln Gln Gln Pro Leu Ala Gly Ser
            500             505             510
Arg Arg Asn Gln Glu Ser Asn Phe Asn Leu Thr His Tyr Gly Thr Gln
            515             520             525
Gln Ile Pro Pro Ala Tyr Lys Asp Leu Ala Glu Pro Trp Ile Gln Val
            530             535             540
Phe Gly Met Glu Leu Val Gly Cys Leu Phe Ser Arg Asn Trp Asn Val
545             550             555             560
Arg Glu Met Ala Leu Arg Arg Leu Ser His Asp Val Ser Gly Ala Leu
            565             570             575
Leu Leu Ala Asn Gly Glu Ser Thr Gly Asn Ser Gly Gly Ser Ser Gly
            580             585             590
Ser Ser Pro Ser Gly Gly Ala Thr Ser Gly Ser Ser Gln Thr Ser Ile
            595             600             605
Ser Gly Asp Val Val Glu Ala Cys Cys Ser Val Leu Ser Met Val Cys
            610             615             620
Ala Asp Pro Val Tyr Lys Val Tyr Val Ala Ala Leu Lys Thr Leu Arg
625             630             635             640
Ala Met Leu Val Tyr Thr Pro Cys His Ser Leu Ala Glu Arg Ile Lys
            645             650             655
Leu Gln Arg Leu Leu Gln Pro Val Val Asp Thr Ile Leu Val Lys Cys
            660             665             670
Ala Asp Ala Asn Ser Arg Thr Ser Gln Leu Ser Ile Ser Thr Leu Leu
            675             680             685
Glu Leu Cys Lys Gly Gln Ala Gly Glu Leu Ala Val Gly Arg Glu Ile
            690             695             700
Leu Lys Ala Gly Ser Ile Gly Ile Gly Gly Val Asp Tyr Val Leu Asn
705             710             715             720
Cys Ile Leu Gly Asn Gln Thr Glu Ser Asn Asn Trp Gln Glu Leu Leu
            725             730             735
Gly Arg Leu Cys Leu Ile Asp Arg Leu Leu Leu Glu Phe Pro Ala Glu
            740             745             750
Phe Tyr Pro His Ile Val Ser Thr Asp Val Ser Gln Ala Glu Pro Val
            755             760             765
Glu Ile Arg Tyr Lys Lys Leu Leu Ser Leu Leu Thr Phe Ala Leu Gln
            770             775             780
Ser Ile Asp Asn Ser His Ser Met Val Gly Lys Leu Ser Arg Arg Ile
785             790             795             800
Tyr Leu Ser Ser Ala Arg Met Val Thr Thr Val Pro His Val Phe Ser
            805             810             815
Lys Leu Leu Glu Met Leu Ser Val Ser Ser Val Ser Thr His Phe Thr
            820             825             830
Arg Met Arg Arg Arg Leu Met Ala Tyr Ala Asp Glu Val Glu Ile Ala
            835             840             845
Glu Ala Ile Gln Leu Gly Val Glu Asp Thr Leu Gln Arg Gln Gln His
            850             855             860
Asn Ser Phe Cys Arg His Leu Phe Pro Thr Thr Ile Trp Lys Pro Gln
865             870             875             880
Arg Thr Val Pro Leu Glu Cys Thr Val His Leu Glu Lys Thr Gly Lys
            885             890             895
Gly Leu Cys Ala Thr Lys Leu Ser Ala Ser Ser Glu Asp Ile Ser Glu
            900             905             910
Arg Leu Ala Arg Ile Ser Val Gly Pro Ser Ser Ser Thr Thr Thr Thr
            915             920             925
Thr Thr Thr Thr Glu Gln Pro Lys Pro Met Val Gln Thr Lys Gly Arg
            930             935             940
Pro His Ser Gln Cys Leu Asn Ser Ser Pro Leu Ser His His Ser Gln
945             950             955             960
Leu Met Phe Pro Ala Leu Ser Thr Pro Ser Ser Ser Thr Pro Ser Val
            965             970             975
```

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```
Pro Ala Gly Thr Ala Thr Asp Val Ser Lys His Arg Leu Gln Gly Phe
        980                 985                 990
Ile Pro Cys Arg Ile Pro Ser Ala Ser Pro Gln Thr Gln Arg Lys Phe
        995                 1000                1005
Ser Leu Gln Phe His Arg Asn Cys Pro Glu Asn Lys Asp Ser Asp Lys
    1010                1015                1020
Leu Ser Pro Val Phe Thr Gln Ser Arg Pro Leu Pro Ser Ser Asn Ile
1025                1030                1035                1040
His Arg Pro Lys Pro Ser Arg Pro Thr Pro Gly Asn Thr Ser Lys Gln
            1045                1050                1055
Gly Asp Pro Ser Lys Asn Ser Met Thr Leu Asp Leu Asn Ser Ser Ser
            1060                1065                1070
Lys Cys Asp Asp Ser Phe Gly Leu Ser Ser Asn Ser Ser Asn Cys Cys
            1075                1080                1085
Tyr Thr Ser Asp Glu Thr Val Phe Thr Pro Val Glu Glu Lys Cys Arg
    1090                1095                1100
Leu Asp Val Asn Thr Glu Leu Asn Ser Ser Ile Glu Asp Leu Leu Glu
1105                1110                1115                1120
Ala Ser Met Pro Ser Ser Asp Thr Thr Val Thr Phe Lys Ser Glu Val
            1125                1130                1135
Ala Val Leu Ser Pro Glu Lys Ala Glu Asn Asp Asp Thr Tyr Lys Asp
            1140                1145                1150
Asp Val Asn His Asn Gln Lys Cys Lys Glu Lys Met Glu Ala Glu Glu
        1155                1160                1165
Glu Glu Ala Leu Ala Ile Ala Met Ala Met Ser Ala Ser Gln Val Ala
    1170                1175                1180
Leu Pro Ile Val Pro Gln Leu Gln Val Glu Asn Gly Glu Asp Ile Ile
1185                1190                1195                1200
Ile Ile Gln Gln Asp Thr Pro Glu Thr Leu Pro Gly His Thr Lys Ala
            1205                1210                1215
Lys Gln Pro Tyr Arg Glu Asp Thr Glu Trp Leu Lys Gly Gln Gln Ile
            1220                1225                1230
Gly Leu Gly Ala Phe Ser Ser Cys Tyr Gln Ala Gln Asp Val Gly Thr
        1235                1240                1245
Gly Thr Leu Met Ala Val Lys Gln Val Thr Tyr Val Arg Asn Thr Ser
    1250                1255                1260
Ser Glu Gln Glu Glu Val Val Glu Ala Leu Arg Glu Glu Ile Arg Met
1265                1270                1275                1280
Met Ser His Leu Asn His Pro Asn Ile Ile Arg Met Leu Gly Ala Thr
            1285                1290                1295
Cys Glu Lys Ser Asn Tyr Asn Leu Phe Ile Glu Trp Met Ala Gly Gly
            1300                1305                1310
Ser Val Ala His Leu Leu Ser Lys Tyr Gly Ala Phe Lys Glu Ser Val
        1315                1320                1325
Val Ile Asn Tyr Thr Glu Gln Leu Leu Arg Gly Leu Ser Tyr Leu His
        1330                1335                1340
Glu Asn Gln Ile Ile His Arg Asp Val Lys Gly Ala Asn Leu Leu Ile
1345                1350                1355                1360
Asp Ser Thr Gly Gln Arg Leu Arg Ile Ala Asp Phe Gly Ala Ala Ala
            1365                1370                1375
Arg Leu Ala Ser Lys Gly Thr Gly Ala Gly Glu Phe Gln Gly Gln Leu
            1380                1385                1390
Leu Gly Thr Ile Ala Phe Met Ala Pro Glu Val Leu Arg Gly Gln Gln
        1395                1400                1405
Tyr Gly Arg Ser Cys Asp Val Trp Ser Val Gly Cys Ala Ile Ile Glu
    1410                1415                1420
Met Ala Cys Ala Lys Pro Pro Trp Asn Ala Glu Lys His Ser Asn His
1425                1430                1435                1440
Leu Ala Leu Ile Phe Lys Ile Ala Ser Ala Thr Thr Ala Pro Ser Ile
            1445                1450                1455
```

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```
Pro Ser His Leu Ser Pro Gly Leu Arg Asp Val Ala Leu Arg Cys Leu
          1460                1465                1470
Glu Leu Gln Pro Gln Asp Arg Pro Pro Ser Arg Glu Leu Leu Lys His
          1475                1480                1485
Pro Val Phe Arg Thr Thr Trp
    1490                1495
```

<210> 16
<211> 37
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:/note =
      synthetic construct

<400> 16
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tggggtcact cttaacgcag tgtaaaaggt aagccct                             37
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<210> 17
<211> 2348
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:/note =
      synthetic construct

<400> 17
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ccgccgccg ggccccggc atgcagcccc ggctgcggag gtgacactca cggaccttag     60
ccaccgccgc cgccatcgcc accatggacg aacaggaggc attgaactca atcatgaacg    120
atctggtggc cctccagatg aaccgacgtc accggatgcc tggatatgag accatgaaga    180
acaaagacac aggtcactca aataggcaga gtgacgtcag aatcaagttc gagcacaacg    240
gggagaggcg aatttatagcg ttcagccggc ctgtgaaata tgaagatgtg gagcacaagg   300
tgacaacagt atttggacaa cctcttgatc tacattacat gaacaatgag ctctccatcc    360
tgctgaaaaa ccaagatgat cttgataaag caattgacat tttagataga agctcaagca    420
tgaaaagcct taggatattg ctgttgtccc aggacagaaa ccataacagt tcctctcccc    480
actctgaggt gtccagacag gtgcggatca aggcttccca gtccgcaggg gatataaata    540
ctatctacca gccccccgag cccagaagca ggcacctctc tgtcagctcc cagaaccctg    600
gccgaagctc acctcccct ggctatgttc ctgagcggca gcagcacatt gcccggcagg    660
ggtcctacac cagcatcaac agtgaggggg agttcatccc agagaccagc gagcagtgca    720
tgctggatcc cctgagcagt gcagaaaatt ccttgtctgg aagctgccaa tccttggaca    780
ggtcagcaga cagcccatcc ttccggaaat cacgaatgtc ccgtgcccag agcttccctg    840
acaacagaca ggaatactca gatcgggaaa ctcagcttta tgacaaaggg gtcaaaggtg    900
gaacctaccc ccggcgctac cacgtgtctg tgcaccacaa ggactacagt gatggcagaa    960
gaacatttcc ccgaatacgg cgtcatcaag gcaacttgtt caccctggtg ccctccagcc   1020
gctccctgag cacaaatggc gagaacatgg gtctggctgt gcaatacctg gaccccgtg    1080
ggcgcctgcg gagtgcggac agcgagaatg ccctctctgt gcaggagagg aatgtgccaa    1140
ccaagtctcc cagtgccccc atcaactggc gccggggaaa gctcctgggc cagggtgcct    1200
tcggcagggt ctatttgtgc tatgacgtgg acacgggacg tgaacttgct tccaagcagg    1260
tccaatttga tccagacagt cctgagacaa gcaaggaggt gagtgctctg gagtgcgaga    1320
tccagttgct aaagaacttg cagcatgagc gcatcgtgca gtactatggc tgtctgcggg    1380
accgcgctga gaagaccctg accatcttca tggagtacat gccagggggc tcggtgaaag    1440
accagttgaa ggcttacggt gctctgacag agagcgtgac ccgaaagtac acgcggcaga    1500
tcctggaggg catgtcctac ctgcacagca acatgattgt tcaccgggac attaagggag    1560
ccaacatcct ccgagactct gctgggaatg taaagctggg ggactttggg gccagcaaac   1620
gcctgcagac gatctgtatg tcggggacgg gcatgcgctc cgtcactggc acaccctact    1680
ggatgagccc tgaggtgatc agcggcgagg gctatggaag gaaagcagac gtgtggagcc    1740
tgggctgcac tgtggtggag atgctgacag agaaaccacc gtgggcagag tatgaagcta    1800
.tggccgccat cttcaagatt gccacccagc. ccaccaatcc tcagctgccc tcccacatct   1860
ctgaacatgg ccgggacttc ctgaggcgca ttttgtggga ggctcgccag agaccttcag    1920
```

```
ctgaggagct gctcacacac cactttgcac agctcatgta ctgagctctc acggccacac   1980
agctgccggt cgccctttgc tgcatggcag ggggctgctg ctgggctcag tgaagttgct   2040
gcttctccca ggcaaggctg tggaccatgg agtggcagcc cagccagcgt cggtctgtgc   2100
cccttccgcc actgggctc agagccgggg tggggtggct gcagcctcag gactgggagc   2160
ccccagcctg tcagatccag gagctccagt gtcctgagct cagcgtggag gggtaggggc   2220
tgggaacagt gtgcaaggca gccgtgggcc ccaccctcgg ggatgtgtcc tgacactgca   2280
attggcaccg aagcccagag ggtctggggg cacaagactg acgccagggt atgaagagtg   2340
ttattttc                                                          2348
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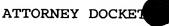
<210> 18
<211> 626
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:/note =
      synthetic construct

<400> 18
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Met Asp Glu Gln Glu Ala Leu Asn Ser Ile Met Asn Asp Leu Val Ala
1               5                   10                  15
Leu Gln Met Asn Arg Arg His Arg Met Pro Gly Tyr Glu Thr Met Lys
            20                  25                  30
Asn Lys Asp Thr Gly His Ser Asn Arg Gln Ser Asp Val Arg Ile Lys
        35                  40                  45
Phe Glu His Asn Gly Glu Arg Arg Ile Ile Ala Phe Ser Arg Pro Val
    50                  55                  60
Lys Tyr Glu Asp Val Glu His Lys Val Thr Thr Val Phe Gly Gln Pro
65                  70                  75                  80
Leu Asp Leu His Tyr Met Asn Asn Glu Leu Ser Ile Leu Leu Lys Asn
                85                  90                  95
Gln Asp Asp Leu Asp Lys Ala Ile Asp Ile Leu Asp Arg Ser Ser Ser
            100                 105                 110
Met Lys Ser Leu Arg Ile Leu Leu Leu Ser Gln Asp Arg Asn His Asn
        115                 120                 125
Ser Ser Ser Pro His Ser Glu Val Ser Arg Gln Val Arg Ile Lys Ala
    130                 135                 140
Ser Gln Ser Ala Gly Asp Ile Asn Thr Ile Tyr Gln Pro Pro Glu Pro
145                 150                 155                 160
Arg Ser Arg His Leu Ser Val Ser Ser Gln Asn Pro Gly Arg Ser Ser
                165                 170                 175
Pro Pro Pro Gly Tyr Val Pro Glu Arg Gln Gln His Ile Ala Arg Gln
            180                 185                 190
Gly Ser Tyr Thr Ser Ile Asn Ser Glu Gly Glu Phe Ile Pro Glu Thr
        195                 200                 205
Ser Glu Gln Cys Met Leu Asp Pro Leu Ser Ser Ala Glu Asn Ser Leu
    210                 215                 220
Ser Gly Ser Cys Gln Ser Leu Asp Arg Ser Ala Asp Ser Pro Ser Phe
225                 230                 235                 240
Arg Lys Ser Arg Met Ser Arg Ala Gln Ser Phe Pro Asp Asn Arg Gln
                245                 250                 255
Glu Tyr Ser Asp Arg Glu Thr Gln Leu Tyr Asp Lys Gly Val Lys Gly
            260                 265                 270
Gly Thr Tyr Pro Arg Arg Tyr His Val Ser Val His His Lys Asp Tyr
        275                 280                 285
Ser Asp Gly Arg Arg Thr Phe Pro Arg Ile Arg Arg His Gln Gly Asn
    290                 295                 300
Leu Phe Thr Leu Val Pro Ser Ser Arg Ser Leu Ser Thr Asn Gly Glu
305                 310                 315                 320
Asn Met Gly Leu Ala Val Gln Tyr Leu Asp Pro Arg Gly Arg Leu Arg
                325                 330                 335
```

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```
Ser Ala Asp Ser Glu Asn Ala Leu Ser Val Gln Glu Arg Asn Val Pro
            340                 345                 350
Thr Lys Ser Pro Ser Ala Pro Ile Asn Trp Arg Arg Gly Lys Leu Leu
        355                 360                 365
Gly Gln Gly Ala Phe Gly Arg Val Tyr Leu Cys Tyr Asp Val Asp Thr
    370                 375                 380
Gly Arg Glu Leu Ala Ser Lys Gln Val Gln Phe Asp Pro Asp Ser Pro
385                 390                 395                 400
Glu Thr Ser Lys Glu Val Ser Ala Leu Glu Cys Glu Ile Gln Leu Leu
                405                 410                 415
Lys Asn Leu Gln His Glu Arg Ile Val Gln Tyr Tyr Gly Cys Leu Arg
            420                 425                 430
Asp Arg Ala Glu Lys Thr Leu Thr Ile Phe Met Glu Tyr Met Pro Gly
        435                 440                 445
Gly Ser Val Lys Asp Gln Leu Lys Ala Tyr Gly Ala Leu Thr Glu Ser
    450                 455                 460
Val Thr Arg Lys Tyr Thr Arg Gln Ile Leu Glu Gly Met Ser Tyr Leu
465                 470                 475                 480
His Ser Asn Met Ile Val His Arg Asp Ile Lys Gly Ala Asn Ile Leu
            485                 490                 495
Arg Asp Ser Ala Gly Asn Val Lys Leu Gly Asp Phe Gly Ala Ser Lys
            500                 505                 510
Arg Leu Gln Thr Ile Cys Met Ser Gly Thr Gly Met Arg Ser Val Thr
        515                 520                 525
Gly Thr Pro Tyr Trp Met Ser Pro Glu Val Ile Ser Gly Glu Gly Tyr
    530                 535                 540
Gly Arg Lys Ala Asp Val Trp Ser Leu Gly Cys Thr Val Val Glu Met
545                 550                 555                 560
Leu Thr Glu Lys Pro Pro Trp Ala Glu Tyr Glu Ala Met Ala Ala Ile
            565                 570                 575
Phe Lys Ile Ala Thr Gln Pro Thr Asn Pro Gln Leu Pro Ser His Ile
            580                 585                 590
Ser Glu His Gly Arg Asp Phe Leu Arg Arg Ile Phe Val Glu Ala Arg
    595                 600                 605
Gln Arg Pro Ser Ala Glu Glu Leu Leu Thr His His Phe Ala Gln Leu
    610                 615                 620
Met Tyr
625
```

```
<210> 19
<211> 1576
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:/note =
      synthetic construct


<400> 19
gaattcgagc cgaccgaccg ctccccggccc gcccccctatg ggccccggct agaggcgccg      60
ccgccgccgg cccgcggagc cccgatgctg gcccggagga agccggtgct gccggcgctc     120
accatcaacc ctaccatcgc cgagggccca tcccctacca gcgagggcgc ctccgaggca     180
aacctggtgg acctgcagaa gaagctggag gagctggaac ttgacgagca gcagaagaag     240
cggctggaag cctttctcac ccagaaagcc aaggttggcg aactcaaaga cgatgacttc     300
gaaaggatct cagagctggg cgcgggcaac ggcggggtgg tcaccaaagt ccagcacaga     360
ccctcgggcc tcatcatggc caggaagctg atccaccttg agatcaagcc ggccatccgg     420
aaccagatca tccgcgagct gcaggtcctg cacgaatgca actcgccgta catcgtgggc     480
ttctacgggg ccttctacag tgacggggag atcagcattt gcatggaaca catggacggc     540
ggctccctgg accaggtgct gaaagaggcc aagaggattc cgaggagat cctggggaaa     600
gtcagcatcg cggttctccg gggcttggcg tacctccgag agaagcacca gatcatgcac     660
```

```
cgagatgtga agccctccaa catcctcgtg aactctagag gggagatcaa gctgtgtgac    720
ttcggggtga gcggccagct catagactcc atggccaact ccttcgtggg cacgcgctcc    780
tacatggctc cggagcggtt gcagggcaca cattactcgg tgcagtcgga catctggagc    840
atgggcctgt ccctggtgga gctggccgtc ggaaggtacc ccatcccccc gcccgacgcc    900
aaagagctgg aggccatctt tggccggccc gtggtcgacg gggaagaagg agagcctcac    960
agcatctcgc ctcggccgag gcccccgggg cgccccgtca gcggtcacgg gatggatagc   1020
cggcctgcca tggccatctt tgaactcctg gactatattg tgaacgagcc acctcctaag   1080
ctgcccaacg gtgtgttcac ccccgacttc caggagtttg tcaataaatg cctcatcaag   1140
aacccagcgg agcgggcgga cctgaagatg ctcacaaacc acaccttcat caagcggtcc   1200
gaggtggaag aagtggattt tgccggctgg ttgtgtaaaa ccctgcggct gaaccagccc   1260
ggcacaccca cgcgcaccgc cgtgtgacag tggccgggct ccctgcgtcc cgctggtgac   1320
ctgcccaccg tccctgtcca tgccccgccc ttccagctga ggacacgtgg cgcctccacc   1380
caccctcctg cctcaccctg cggagagcac cgtggcgggg cgacagcgca tgcaggaacg   1440
ggggtctcct ctcctgccag tcctggccgg ggtgcctctg gggacgggcg acgctgctgt   1500
gtgtggtctc agaggctctg cttccttagg ttacaaaaca aaacagggag agaaaagcaa   1560
aaaaaaaaaa aaaaaa                                                    1576
```

<210> 20
<211> 2222
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:/note =
      synthetic construct

<400> 20
```
attcggcacg agggaggaag cgagaggtgc tgccctcccc ccggagttgg aagcgcgtta     60
cccgggtcca aaatgcccaa gaagaagccg acgcccatcc agctgaaccc ggcccccgac    120
ggctctgcag ttaacgggac cagctctgcg gagaccaact tggaggcctt gcagaagaag    180
ctggaggagc tagagcttga tgagcagcag cgaaagcgcc ttgaggcctt tcttacccag    240
aagcagaagg tgggagaact gaaggatgac gactttgaga agatcagtga gctggggct     300
ggcaatggcg gtgtggtgtt caaggtctcc cacaagcctt ctggcctggt catggccaga    360
aagctaattc atctggagat caaacccgca atccggaacc agatcataag ggagctgcag    420
gttctgcatg agtgcaactc tccgtacatc gtgggcttct atggtgcgtt ctacagcgat    480
ggcgagatca gtatctgcat ggagcacatg gatggaggtt ctctggatca agtcctgaag    540
aaagctggaa gaattcctga acaaatttta ggaaaagtta gcattgctgt aataaaaggc    600
ctgacatatc tgagggagaa gcacaagatc atgcacagag atgtcaagcc ctccaacatc    660
ctagtcaact cccgtgggga gatcaagctc tgtgactttg gggtcagcgg gcagctcatc    720
gactccatgg ccaactcctt cgtgggcaca aggtcctaca tgtcgccaga aagactccag    780
gggactcatt actctgtgca gtcagacatc tggagcatgg gactgtctct ggtagagatg    840
gcggttggga ggtatcccat ccctcctcca gatgccaagg agctggagct gatgtttggg    900
tgccaggtgg aaggagatgc ggctgagacc ccacccaggc caaggacccc cgggaggccc    960
cttagctcat acggaatgga cagccgacct cccatggcaa tttttgagtt gttggattac   1020
atagtcaacg agcctcctcc aaaaactgccc agtggagtgt tcagtctgga atttcaagat   1080
tttgtgaata aatgcttaat aaaaaacccc gcagagagag cagatttgaa gcaactcatg   1140
gttcatgctt ttatcaagag atctgatgct gaggaagtgg attttgcagg ttggctctgc   1200
tccaccatcg gccttaacca gcccagcaca ccaacccatg ctgctggcgt ctaagtgttt   1260
gggaagcaac aaagagcgag tccctgccc ggtggtttgc catgtcgctt ttgggcctcc   1320
ttcccatgcc tgtctctgtt cagatgtgca tttcacctgt gacaaaggat gaagaacaca   1380
gcatgtgcca agattctact cttgtcattt ttaatattac tgtctttatt cttattacta   1440
ttattgttcc cctaagtgga ttggctttgt gcttggggct atttgtgtgt atgctgatga   1500
tcaaaacctg tgccaggctg aattacagtg aaatttttgg tgaatgtggg tagtcattct   1560
tacaattgca ctgctgttcc tgctccatga ctggctgtct gcctgtattt tcggactttg   1620
acatttgaca tttggtggac tttatcttgc tgggcatact ttctctctag gagggagcct   1680
tgtgagatcc ttcacaggca gtgcatgtga agcatgcttt gctgctatga aaatgagcat   1740
cagagagtgt acatcatgtt attttattat tattatttgc ttttcatgta gaactcagca   1800
gttgacatcc aaatctagcc agagcccttc actgccatga tagctggggc ttcaccagtc   1860
tgtctactgt ggtgatctgt agacttctgg ttgtatttct atatttattt tcagtatact   1920
gtgtgggata cttagtggta tgtctcttta agttttgatt aatgtttctt aaatggaatt   1980
atttgaatgt cacaaattga tcaagatatt aaaatgtcgg atttatcttt ccccatatcc   2040
```

```
aagtaccaat gctgttgtaa acaacgtgta tagtgcctaa aattgtatga aaatcctttt    2100
aaccatttta acctagatgt ttaacaaatc taatctctta ttctaataaa tatactatga    2160
aataaaaaaa aaaggagaaa gctaaaaaaa aaaaaaaaa aaaaaaaaa aaaaaaaaa       2220
aa                                                                   2222
```

<210> 21
<211> 2371
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:/note =
      synthetic construct

<400> 21
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gcaccgcgcg agcttggctg cttctggggc ctgtgtggcc ctgtgtgtcg gaaagatgga      60
gcaagaagcc gagcccgagg ggcggccgcg acccctctga ccgagatcct gctgctttcg     120
agccaggagc accgtccctc cccggattag tgcgtacgag cgcccagtgc cctggcccgg     180
agagtggaat gatccccgag gcccagggcg tcgtgcttcc gcagtagtca gtccccgtga     240
aggaaactgg ggagtcttga gggacccccg actccaagcg cgaaaacccc ggatggtgag     300
gagcaggcaa atgtgcaata ccaacatgtc tgtacctact gatggtgctg taaccacctc     360
acagattcca gcttcggaac aagagaccct ggttagacca aagccattgc ttttgaagtt     420
attaaagtct gttggtgcac aaaaagacac ttatactatg aaagaggttc ttttttatct     480
tggccagtat attatgacta aacgattata tgatgagaag caacaacata ttgtatattg     540
ttcaaatgat cttctaggag atttgtttgg cgtgccaagc ttctctgtga aagagcacag     600
gaaaatatat accatgatct acaggaactt ggtagtagtc aatcagcagg aatcatcgga     660
ctcaggtaca tctgtgagtg agaacaggtg tcaccttgaa ggtgggagtg atcaaaagga     720
ccttgtacaa gagcttcagg aagagaaacc ttcatcttca catttggttt ctagaccatc     780
tacctcatct agaaggagag caattagtga gacagaagaa aattcagatg aattatctgg     840
tgaacgacaa agaaaacgcc acaaatctga tagtatttcc ctttcctttg atgaaagcct     900
ggctctgtgt gtaataaggg agatatgttg tgaaagaagc agtagcagtg aatctacagg     960
gacgccatcg aatccggatc ttgatgctgg tgtaagtgaa cattcaggtg attggttgga    1020
tcaggattca gtttcagatc agtttagtgt agaatttgaa gttgaatctc tcgactcaga    1080
agattatagc cttagtgaag aaggacaaga actctcagat gaagatgatg aggtatatca    1140
agttactgtg tatcaggcag gggagagtga tacagattca tttgaagaag atcctgaaat    1200
ttccttagct gactattgga aatgcacttc atgcaatgaa atgaatcccc ccttccatc     1260
acattgcaac agatgttggg cccttcgtga gaattggctt cctgaagata aagggaaaga    1320
taaaggggaa atctctgaga aagccaaact ggaaaactca acacaagctg aagagggctt    1380
tgatgttcct gattgtaaaa aaactatagt gaatgattcc agagagtcat gtgttgagga    1440
aaatgatgat aaaattacac aagcttcaca atcacaagaa agtgaagact attctcagcc    1500
atcaacttct agtagcatta tttatagcag ccaagaagat gtgaaagagt ttgaaaggga    1560
agaaacccaa gacaaagaag agagtgtgga atctagtttg ccccttaatg ccattgaacc    1620
ttgtgtgatt tgtcaaggtc gacctaaaaa tggttgcatt gtccatggca aaacaggaca    1680
tcttatggcc tgctttacat gtgcaaagaa gctaaagaaa aggaataagc cctgcccagt    1740
atgtagacaa ccaattcaaa tgattgtgct aacttatttc ccctagttga cctgtctata    1800
agagaattat atatttctaa ctatataacc ctaggaattt agacaacctg aaatttattc    1860
acatatatca aagtgagaaa atgcctcaat tcacatagat ttcttctctt tagtataatt    1920
gacctacttt ggtagtggaa tagtgaatac ttactataat ttgacttgaa tatgtagctc    1980
atcctttaca ccaactccta attttaaata atttctactc tgtcttaaat gagaagtact    2040
tggttttttt tttcttaaat atgtatatga catttaaatg taacttatta ttttttttga    2100
gaccgagtct tgctctgtta cccaggctgg agtgcagtgg gtgatcttgg ctcactgcaa    2160
gctctgccct ccccgggttc gcaccattct cctgcctcag cctcccaatt agcttggcct    2220
acagtcatct gccaccacac ctggctaatt ttttgtactt ttagtagaga cagggtttca    2280
ccgtgttagc caggatggtc tcgatctcct gacctcgtga tccgcccacc tcggcctccc    2340
aaagtgctgg gattacaggc atgagccacc g                                   2371
```
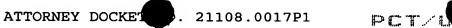
<210> 22
<211> 491
<212> PRT
<213> Artificial Sequence

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<220>
<223> Description of Artificial Sequence:/note =
      synthetic construct

<400> 22
Met Cys Asn Thr Asn Met Ser Val Pro Thr Asp Gly Ala Val Thr Thr
1               5                   10                  15
Ser Gln Ile Pro Ala Ser Glu Gln Glu Thr Leu Val Arg Pro Lys Pro
            20                  25                  30
Leu Leu Leu Lys Leu Leu Lys Ser Val Gly Ala Gln Lys Asp Thr Tyr
        35                  40                  45
Thr Met Lys Glu Val Leu Phe Tyr Leu Gly Gln Tyr Ile Met Thr Lys
    50                  55                  60
Arg Leu Tyr Asp Glu Lys Gln Gln His Ile Val Tyr Cys Ser Asn Asp
65                  70                  75                  80
Leu Leu Gly Asp Leu Phe Gly Val Pro Ser Phe Ser Val Lys Glu His
                85                  90                  95
Arg Lys Ile Tyr Thr Met Ile Tyr Arg Asn Leu Val Val Val Asn Gln
            100                 105                 110
Gln Glu Ser Ser Asp Ser Gly Thr Ser Val Ser Glu Asn Arg Cys His
        115                 120                 125
Leu Glu Gly Gly Ser Asp Gln Lys Asp Leu Val Gln Glu Leu Gln Glu
    130                 135                 140
Glu Lys Pro Ser Ser Ser His Leu Val Ser Arg Pro Ser Thr Ser Ser
145                 150                 155                 160
Arg Arg Arg Ala Ile Ser Glu Thr Glu Glu Asn Ser Asp Glu Leu Ser
                165                 170                 175
Gly Glu Arg Gln Arg Lys Arg His Lys Ser Asp Ser Ile Ser Leu Ser
            180                 185                 190
Phe Asp Glu Ser Leu Ala Leu Cys Val Ile Arg Glu Ile Cys Cys Glu
        195                 200                 205
Arg Ser Ser Ser Ser Glu Ser Thr Gly Thr Pro Ser Asn Pro Asp Leu
    210                 215                 220
Asp Ala Gly Val Ser Glu His Ser Gly Asp Trp Leu Asp Gln Asp Ser
225                 230                 235                 240
Val Ser Asp Gln Phe Ser Val Glu Phe Glu Val Glu Ser Leu Asp Ser
                245                 250                 255
Glu Asp Tyr Ser Leu Ser Glu Glu Gly Gln Glu Leu Ser Asp Glu Asp
            260                 265                 270
Asp Glu Val Tyr Gln Val Thr Val Tyr Gln Ala Gly Glu Ser Asp Thr
        275                 280                 285
Asp Ser Phe Glu Glu Asp Pro Glu Ile Ser Leu Ala Asp Tyr Trp Lys
    290                 295                 300
Cys Thr Ser Cys Asn Glu Met Asn Pro Pro Leu Pro Ser His Cys Asn
305                 310                 315                 320
Arg Cys Trp Ala Leu Arg Glu Asn Trp Leu Pro Glu Asp Lys Gly Lys
                325                 330                 335
Asp Lys Gly Glu Ile Ser Glu Lys Ala Lys Leu Glu Asn Ser Thr Gln
            340                 345                 350
Ala Glu Glu Gly Phe Asp Val Pro Asp Cys Lys Lys Thr Ile Val Asn
        355                 360                 365
Asp Ser Arg Glu Ser Cys Val Glu Glu Asn Asp Asp Lys Ile Thr Gln
    370                 375                 380
Ala Ser Gln Ser Gln Glu Ser Glu Asp Tyr Ser Gln Pro Ser Thr Ser
385                 390                 395                 400
Ser Ser Ile Ile Tyr Ser Ser Gln Glu Asp Val Lys Glu Phe Glu Arg
                405                 410                 415
Glu Glu Thr Gln Asp Lys Glu Glu Ser Val Glu Ser Ser Leu Pro Leu
            420                 425                 430
```

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```
Asn Ala Ile Glu Pro Cys Val Ile Cys Gln Gly Arg Pro Lys Asn Gly
        435                 440                 445
Cys Ile Val His Gly Lys Thr Gly His Leu Met Ala Cys Phe Thr Cys
        450                 455                 460
Ala Lys Lys Leu Lys Lys Arg Asn Lys Pro Cys Pro Val Cys Arg Gln
465                 470                 475                 480
Pro Ile Gln Met Ile Val Leu Thr Tyr Phe Pro
                485                 490
```

<210> 23
<211> 1599
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:/note =
      synthetic construct

<400> 23

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gagactgtgc cctgtccacg gtgcctcctg catgtcctgc tgccctgagc tgtcccgagc      60
taggtgacag cgtaccacgc tgccaccatg aatgaggtgt ctgtcatcaa agaaggctgg     120
ctccacaagc gtggtgaata catcaagacc tggaggccac ggtacttcct gctgaagagc     180
gacggctcct tcattgggta caaggagagg cccgaggccc ctgatcagac tctaccccc      240
ttaaacaact tctccgtagc agaatgccag ctgatgaaga ccgagaggcc gcgacccaac     300
acctttgtca tacgctgcct gcagtggacc acagtcatcg agaggacctt ccacgtggat     360
tctccagacg agagggagga gtggatgcgg gccatccaga tggtcgccaa cagcctcaag     420
cagcgggccc caggcgagga ccccatggac tacaagtgtg gctcccccag tgactcctcc     480
acgactgagg agatggaagt ggcggtcagc aaggcacggg ctaaagtgac catgaatgac     540
ttcgactatc tcaaactcct tggcaaggga acctttggca aagtcatcct ggtgcgggag     600
aaggccactg gccgctacta cgccatgaag atcctgcgaa aggaagtcat cattgccaag     660
gatgaagtcg ctcacacagt caccgagagc cgggtcctcc agaacaccag gcacccgttc     720
ctcactgcgc tgaagtatgc cttccagacc cacgaccgcc tgtgctttgt gatggagtat     780
gccaacgggg gtgagctgtt cttccacctg tcccgggagc gtgtcttcac agaggagcgg     840
gcccggtttt atggtgcaga gattgtctcg gctcttgagt acttgcactc gcgggacgtg     900
gtataccgcg acatcaagct ggaaaacctc atgctggaca agatggcca catcaagatc     960
actgactttg gcctctgcaa agagggcatc agtgacgggg ccaccatgaa aaccttctgt    1020
gggacccccg gagtacctgg cgcctgaggtg ctggaggaca atgactatgg ccgggccgtg    1080
gactggtggg ggctgggtgt ggtcatgtac gagatgatgt gcggccgcct gcccttctac    1140
aaccaggacc acgagcgcct cttcgagctc atcctcatgg aagagatccg cttcccgcgc    1200
acgctcagcc ccgaggccaa gtccctgctt gctgggctgc ttaagaagga ccccaagcag    1260
aggcttggtg gggggcccag cgatgccaag gaggtcatgg agcacaggtt cttcctcagc    1320
atcaactggc aggacgtggt ccagaagaag ctcctgccac ccttcaaacc tcaggtcacg    1380
tccgaggtcg acacaaggta cttcgatgat gaatttaccg cccagtccat cacaatcaca    1440
cccctgacc gctatgacag cctgggctta ctggagctgg accagcggac ccacttcccc    1500
cagttctcct actcggccag catccgcgag tgagcagtct gcccacgcag aggacgcacg    1560
ctcgctgcca tcaccgctgg gtggtttttt accctgcc                           1599
```

<210> 24
<211> 481
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:/note =
      synthetic construct

<400> 24

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Met Asn Glu Val Ser Val Ile Lys Glu Gly Trp Leu His Lys Arg Gly
1               5                   10                  15
Glu Tyr Ile Lys Thr Trp Arg Pro Arg Tyr Phe Leu Leu Lys Ser Asp
            20                  25                  30
```

```
Gly Ser Phe Ile Gly Tyr Lys Glu Arg Pro Glu Ala Pro Asp Gln Thr
        35              40              45
Leu Pro Pro Leu Asn Asn Phe Ser Val Ala Glu Cys Gln Leu Met Lys
    50              55              60
Thr Glu Arg Pro Arg Pro Asn Thr Phe Val Ile Arg Cys Leu Gln Trp
65              70              75              80
Thr Thr Val Ile Glu Arg Thr Phe His Val Asp Ser Pro Asp Glu Arg
            85              90              95
Glu Glu Trp Met Arg Ala Ile Gln Met Val Ala Asn Ser Leu Lys Gln
            100             105             110
Arg Ala Pro Gly Glu Asp Pro Met Asp Tyr Lys Cys Gly Ser Pro Ser
        115             120             125
Asp Ser Ser Thr Thr Glu Glu Met Glu Val Ala Val Ser Lys Ala Arg
    130             135             140
Ala Lys Val Thr Met Asn Asp Phe Asp Tyr Leu Lys Leu Leu Gly Lys
145             150             155             160
Gly Thr Phe Gly Lys Val Ile Leu Val Arg Glu Lys Ala Thr Gly Arg
            165             170             175
Tyr Tyr Ala Met Lys Ile Leu Arg Lys Glu Val Ile Ile Ala Lys Asp
            180             185             190
Glu Val Ala His Thr Val Thr Glu Ser Arg Val Leu Gln Asn Thr Arg
        195             200             205
His Pro Phe Leu Thr Ala Leu Lys Tyr Ala Phe Gln Thr His Asp Arg
    210             215             220
Leu Cys Phe Val Met Glu Tyr Ala Asn Gly Gly Glu Leu Phe Phe His
225             230             235             240
Leu Ser Arg Glu Arg Val Phe Thr Glu Glu Arg Ala Arg Phe Tyr Gly
            245             250             255
Ala Glu Ile Val Ser Ala Leu Glu Tyr Leu His Ser Arg Asp Val Val
            260             265             270
Tyr Arg Asp Ile Lys Leu Glu Asn Leu Met Leu Asp Lys Asp Gly His
        275             280             285
Ile Lys Ile Thr Asp Phe Gly Leu Cys Lys Glu Gly Ile Ser Asp Gly
    290             295             300
Ala Thr Met Lys Thr Phe Cys Gly Thr Pro Glu Tyr Leu Ala Pro Glu
305             310             315             320
Val Leu Glu Asp Asn Asp Tyr Gly Arg Ala Val Asp Trp Trp Gly Leu
            325             330             335
Gly Val Val Met Tyr Glu Met Met Cys Gly Arg Leu Pro Phe Tyr Asn
            340             345             350
Gln Asp His Glu Arg Leu Phe Glu Leu Ile Leu Met Glu Glu Ile Arg
        355             360             365
Phe Pro Arg Thr Leu Ser Pro Glu Ala Lys Ser Leu Leu Ala Gly Leu
    370             375             380
Leu Lys Lys Asp Pro Lys Gln Arg Leu Gly Gly Gly Pro Ser Asp Ala
385             390             395             400
Lys Glu Val Met Glu His Arg Phe Phe Leu Ser Ile Asn Trp Gln Asp
            405             410             415
Val Val Gln Lys Lys Leu Leu Pro Pro Phe Lys Pro Gln Val Thr Ser
            420             425             430
Glu Val Asp Thr Arg Tyr Phe Asp Asp Glu Phe Thr Ala Gln Ser Ile
        435             440             445
Thr Ile Thr Pro Pro Asp Arg Tyr Asp Ser Leu Gly Leu Leu Glu Leu
    450             455             460
Asp Gln Arg Thr His Phe Pro Gln Phe Ser Tyr Ser Ala Ser Ile Arg
465             470             475             480
Glu
```

<210> 25
<211> 1547

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<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:/note =
      synthetic construct

<400> 25
gggagtcatc atgagcgatg ttaccattgt gaaagaaggt tgggttcaga agaggggaga      60
atatataaaa aactggaggc caagatactt ccttttgaag acagatggct cattcatagg     120
atataaagag aaacctcaag atgtggattt accttatccc ctcaacaact tttcagtggc     180
aaaatgccag ttaatgaaaa cagaacgacc aaagccaaac acatttataa tcagatgtct     240
ccagtggact actgttatag agagaacatt tcatgtagat actccagagg aaagggaaga     300
atggacagaa gctatccagg ctgtagcaga cagactgcag aggcaagaag aggagagaat     360
gaattgtagt ccaacttcac aaaattgataa tataggagag gaagagatgg atgcctctac     420
aacccatcat aaaagaaaga caatgaatga ttttgactat ttgaaactac taggtaaagg     480
cactttgggg aaagttattt tggttcgaga gaaggcaagt ggaaaatact atgctatgaa     540
gattctgaag aaagaagtca ttattgcaaa ggatgaagtg gcacacactc taactgaaag     600
cagagtatta aagaacacta gacatccctt tttaacatcc ttgaaatatt ccttccagac     660
aaaagaccgt ttgtgttttg tgatggaata tgttaatggg ggcgagctgt ttttccattt     720
gtcgagagag cgggtgttct ctgaggaccg cacacgtttc tatggtgcag aaattgtctc     780
tgccttggac tatctacatt ccggaaagat tgtgtaccgt gatctcaagt tggagaatct     840
aatgctggac aaagatggcc acataaaaat tacagatttt ggactttgca agaagggat     900
cacagatgca gccaccatga agacattctg tggcactcca gaatatctgg caccagaggt     960
gttagaagat aatgactatg gccgagcagt agactggtgg ggcctagggg ttgtcatgta    1020
tgaaatgatg tgtgggaggt tacctttcta caaccaggac catgagaaac tttttgaatt    1080
aatattaatg gaagacatta aatttcctcg aacactctct tcagatgcaa aatcattgct    1140
ttcagggctc ttgataaagg atccaaataa acgccttggt ggaggaccag atgatgcaaa    1200
agaaattatg agacacagtt tcttctctgg agtaaactgg caagatgtat atgataaaaa    1260
gcttgtacct cctttaaac ctcaagtaac atctgagaca gatactagat attttgatga    1320
agaatttaca gctcagacta ttacaataac accacctgaa aaatatgatg aggatggtat    1380
ggactgcatg gacaatgaga ggcggccgca tttccctcaa ttttcctact ctgcaagtgg    1440
acgagaataa gtctctttca ttctgctact tcactgtcat cttcaattta ttactgaaaa    1500
tgattcctgg acatcaccag tcctagctct tacacatagc aggggca                 1547
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<210> 26
<211> 479
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:/note =
      synthetic construct

<400> 26
Met Ser Asp Val Thr Ile Val Lys Glu Gly Trp Val Gln Lys Arg Gly
1               5                   10                  15
Glu Tyr Ile Lys Asn Trp Arg Pro Arg Tyr Phe Leu Leu Lys Thr Asp
            20                  25                  30
Gly Ser Phe Ile Gly Tyr Lys Glu Lys Pro Gln Asp Val Asp Leu Pro
        35                  40                  45
Tyr Pro Leu Asn Asn Phe Ser Val Ala Lys Cys Gln Leu Met Lys Thr
    50                  55                  60
Glu Arg Pro Lys Pro Asn Thr Phe Ile Ile Arg Cys Leu Gln Trp Thr
65                  70                  75                  80
Thr Val Ile Glu Arg Thr Phe His Val Asp Thr Pro Glu Glu Arg Glu
                85                  90                  95
Glu Trp Thr Glu Ala Ile Gln Ala Val Ala Asp Arg Leu Gln Arg Gln
            100                 105                 110
Glu Glu Glu Arg Met Asn Cys Ser Pro Thr Ser Gln Ile Asp Asn Ile
        115                 120                 125
```
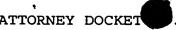
30

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Gly Glu Glu Glu Met Asp Ala Ser Thr Thr His His Lys Arg Lys Thr
    130                 135                 140
Met Asn Asp Phe Asp Tyr Leu Lys Leu Leu Gly Lys Gly Thr Phe Gly
145                 150                 155                 160
Lys Val Ile Leu Val Arg Glu Lys Ala Ser Gly Lys Tyr Tyr Ala Met
                165                 170                 175
Lys Ile Leu Lys Lys Glu Val Ile Ile Ala Lys Asp Glu Val Ala His
                180                 185                 190
Thr Leu Thr Glu Ser Arg Val Leu Lys Asn Thr Arg His Pro Phe Leu
            195                 200                 205
Thr Ser Leu Lys Tyr Ser Phe Gln Thr Lys Asp Arg Leu Cys Phe Val
    210                 215                 220
Met Glu Tyr Val Asn Gly Gly Glu Leu Phe Phe His Leu Ser Arg Glu
225                 230                 235                 240
Arg Val Phe Ser Glu Asp Arg Thr Arg Phe Tyr Gly Ala Glu Ile Val
                245                 250                 255
Ser Ala Leu Asp Tyr Leu His Ser Gly Lys Ile Val Tyr Arg Asp Leu
                260                 265                 270
Lys Leu Glu Asn Leu Met Leu Asp Lys Asp Gly His Ile Lys Ile Thr
            275                 280                 285
Asp Phe Gly Leu Cys Lys Glu Gly Ile Thr Asp Ala Ala Thr Met Lys
    290                 295                 300
Thr Phe Cys Gly Thr Pro Glu Tyr Leu Ala Pro Glu Val Leu Glu Asp
305                 310                 315                 320
Asn Asp Tyr Gly Arg Ala Val Asp Trp Trp Gly Leu Gly Val Val Met
                325                 330                 335
Tyr Glu Met Met Cys Gly Arg Leu Pro Phe Tyr Asn Gln Asp His Glu
                340                 345                 350
Lys Leu Phe Glu Leu Ile Leu Met Glu Asp Ile Lys Phe Pro Arg Thr
            355                 360                 365
Leu Ser Ser Asp Ala Lys Ser Leu Leu Ser Gly Leu Leu Ile Lys Asp
    370                 375                 380
Pro Asn Lys Arg Leu Gly Gly Gly Pro Asp Asp Ala Lys Glu Ile Met
385                 390                 395                 400
Arg His Ser Phe Phe Ser Gly Val Asn Trp Gln Asp Val Tyr Asp Lys
                405                 410                 415
Lys Leu Val Pro Pro Phe Lys Pro Gln Val Thr Ser Glu Thr Asp Thr
                420                 425                 430
Arg Tyr Phe Asp Glu Glu Phe Thr Ala Gln Thr Ile Thr Ile Thr Pro
            435                 440                 445
Pro Glu Lys Tyr Asp Glu Asp Gly Met Asp Cys Met Asp Asn Glu Arg
    450                 455                 460
Arg Pro His Phe Pro Gln Phe Ser Tyr Ser Ala Ser Gly Arg Glu
465                 470                 475
```

```
<210> 27
<211> 2277
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:/note =
      synthetic construct

<400> 27
ctctgggggt gctgctgagc gaggcgagag gcagcctcct cctctcggcc agaggcagga      60
gcgaggcgag cgcggggaag gcaggccggc agcccgtgtg agccccatgc ggcgagcgcc     120
tgcgagaagg ggaggaggag ccggcccgcc gcccgccgcc cggggatggt gaggaggcgg     180
cgctgcgtga gcccagttag gccttcgctc gggcccgccg ccagctctcc cttcctccgc     240
tcgctcgctc cccccttccc tctccttccc tgccgccgcc gccgccgccc tcccatcacc     300
tcctccccgg gctcccgcag ccataagtag ctgagaagga gaaagacaag aaaaagaaca     360
```

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tcccttttgt ggacccttct gctggagttc aggaatttca acggtgatct tttgactgat    420
ccaccagcct gataaactga tccaccaaga gacattcccg ccattatgaa tgaagtagcg    480
atagtgaagg aaggatggct ccacaaacga ggagaatata tcaaaacatg gaggccacgg    540
tattttcttt taaagaatga tggcacattc attggctaca aggaacgacc gcaagacgtt    600
gaccaacgag aatcaccttt aaataacttc tcagtagctc agtgccagct gatgaagaca    660
gaacgaccta aaccaaacac atttatcatt agatgcctcc agtggaccac agtaattgaa    720
agaacatttc atgtggagac tccagaggag cgggaagaat ggacaaaagc tatccaaact    780
gttgcagaca gcctcaagaa acaggaggaa gagatgatgg atttagatc tggttctcct    840
agtgataatt caggtgctga agaaatggaa gtttctatga caaagccaaa acacaaagtg    900
accatgaatg aatttgaata ccttaagcta ctgggaaaag cactttggg aaaggtcatt    960
ttagttaaag aaaaagcaac cggacggtat tatgctatga aaattctgaa gaaggaagtt   1020
attgtagcaa aggatgaagt agcacacacg ctgacagaaa accgtgtttt acagaactca   1080
cggcatccat tcttaacagc tttaaagtat tcctttcaga cacacgatcg cttgtgtttt   1140
gttatggagt atgctaacgg aggggagttg ttttccatc tgtcgagaga gcgtgtattt   1200
tctgaagacc gggcgcgttt ttatggggct gagattgttt cagcgctgga ttacctgcat   1260
tcagagaaga atgtggtgta cagagatttg aagctggaaa atcttatgct ggataaagac   1320
gggcacataa aaattacaga ctttggacta tgtaaagaag gcataaaaga tggagcaaca   1380
atgaagactt tctgtggcac tccagagtat cttgcaccag aggtgctgga ggataatgac   1440
tatggtcgtg cagtggactg gtggggatta ggagttgtga tgtatgaaat gatgtgtggc   1500
cggctccctt ctacaatca ggaccatgaa aagctctttg aactcatcct tatggaagag   1560
attagatttc cacgcacttt gtcacctgaa gcaaaatctc tcttgtcagg tttgctgaag   1620
aaagatccta agcaaaggtt aggaggcggt cctgatgatg ccaaggagat tatgcagcac   1680
aaattctttg ctggcattgt ttggcaagat gtatacggga agaagcttgt acctccattt   1740
aagccacaag ttacatctga aacagataca agatactttg atgaagaatt tacagcacag   1800
atgattacaa tcactcctcc tgaccaagat gacagcatgg attgtgtaga caatgagaga   1860
agacctcatt ttcctcagtt ctcctattca gccagtggaa ccgcttaatg ttttgcagtg   1920
ttttcccatt cagaaacaaa acagactgca ttttggggac cttacttcaa tggacactag   1980
agaactttct atattatctg aattacaaac tgtgtttgta ttacgattta gatgaatttc   2040
taggaagcct cacagattct gtatttaaaa caattctttg atgcatttt gagaaggaaa   2100
acaaatccat tcttaaagta ttacgtcaag gctcttatgc tgaacgacca taggtttta   2160
agaatatgca ccaaaactgt ttactttaga attaattaag gcattcaata tcagctatag   2220
gatctaatca ttcctgtcaa aagtttaaga ccaggaacct tagagtagaa acgaaac      2277
```

```
<210> 28
<211> 480
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:/note =
      synthetic construct

<400> 28
Met Asn Glu Val Ala Ile Val Lys Glu Gly Trp Leu His Lys Arg Gly
1               5                   10                  15
Glu Tyr Ile Lys Thr Trp Arg Pro Arg Tyr Phe Leu Leu Lys Asn Asp
            20                  25                  30
Gly Thr Phe Ile Gly Tyr Lys Glu Arg Pro Gln Asp Val Asp Gln Arg
        35                  40                  45
Glu Ser Pro Leu Asn Asn Phe Ser Val Ala Gln Cys Gln Leu Met Lys
    50                  55                  60
Thr Glu Arg Pro Lys Pro Asn Thr Phe Ile Ile Arg Cys Leu Gln Trp
65                  70                  75                  80
Thr Thr Val Ile Glu Arg Thr Phe His Val Glu Thr Pro Glu Glu Arg
                85                  90                  95
Glu Glu Trp Thr Lys Ala Ile Gln Thr Val Ala Asp Ser Leu Lys Lys
            100                 105                 110
Gln Glu Glu Glu Met Met Asp Phe Arg Ser Gly Ser Pro Ser Asp Asn
        115                 120                 125
Ser Gly Ala Glu Glu Met Glu Val Ser Met Thr Lys Pro Lys His Lys
    130                 135                 140
```

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Val Thr Met Asn Glu Phe Glu Tyr Leu Lys Leu Leu Gly Lys Gly Thr
145             150                 155                 160
Phe Gly Lys Val Ile Leu Val Lys Glu Lys Ala Thr Gly Arg Tyr Tyr
            165                 170                 175
Ala Met Lys Ile Leu Lys Lys Glu Val Ile Val Ala Lys Asp Glu Val
            180                 185                 190
Ala His Thr Leu Thr Glu Asn Arg Val Leu Gln Asn Ser Arg His Pro
        195                 200                 205
Phe Leu Thr Ala Leu Lys Tyr Ser Phe Gln Thr His Asp Arg Leu Cys
    210                 215                 220
Phe Val Met Glu Tyr Ala Asn Gly Gly Glu Leu Phe Phe His Leu Ser
225                 230                 235                 240
Arg Glu Arg Val Phe Ser Glu Asp Arg Ala Arg Phe Tyr Gly Ala Glu
                245                 250                 255
Ile Val Ser Ala Leu Asp Tyr Leu His Ser Glu Lys Asn Val Val Tyr
            260                 265                 270
Arg Asp Leu Lys Leu Glu Asn Leu Met Leu Asp Lys Asp Gly His Ile
        275                 280                 285
Lys Ile Thr Asp Phe Gly Leu Cys Lys Glu Gly Ile Lys Asp Gly Ala
    290                 295                 300
Thr Met Lys Thr Phe Cys Gly Thr Pro Glu Tyr Leu Ala Pro Glu Val
305                 310                 315                 320
Leu Glu Asp Asn Asp Tyr Gly Arg Ala Val Asp Trp Trp Gly Leu Gly
                325                 330                 335
Val Val Met Tyr Glu Met Met Cys Gly Arg Leu Pro Phe Tyr Asn Gln
            340                 345                 350
Asp His Glu Lys Leu Phe Glu Leu Ile Leu Met Glu Glu Ile Arg Phe
        355                 360                 365
Pro Arg Thr Leu Ser Pro Glu Ala Lys Ser Leu Leu Ser Gly Leu Leu
    370                 375                 380
Lys Lys Asp Pro Lys Gln Arg Leu Gly Gly Gly Pro Asp Asp Ala Lys
385                 390                 395                 400
Glu Ile Met Gln His Lys Phe Phe Ala Gly Ile Val Trp Gln Asp Val
                405                 410                 415
Tyr Gly Lys Lys Leu Val Pro Pro Phe Lys Pro Gln Val Thr Ser Glu
            420                 425                 430
Thr Asp Thr Arg Tyr Phe Asp Glu Glu Phe Thr Ala Gln Met Ile Thr
        435                 440                 445
Ile Thr Pro Pro Asp Gln Asp Asp Ser Met Asp Cys Val Asp Asn Glu
    450                 455                 460
Arg Arg Pro His Phe Pro Gln Phe Ser Tyr Ser Ala Ser Gly Thr Ala
465                 470                 475                 480
```

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